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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:08:12 ; Search time 48 Seconds
(without alignments)
2104.352 Million cell updates/sec

Title: US-10-049-569-2
Perfect score: 1858
Sequence: 1 MGPGALLAGLLVMVLAVAL.....ASTHNGSVTENDSCLQOQH 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	363	9	US-09-736-131-2
2	1858	100.0	363	10	US-09-782-974C-186
3	1858	100.0	363	12	US-10-206-915-590
4	1858	100.0	363	12	US-10-199-670-590
5	1858	100.0	363	12	US-10-201-858-590
6	1858	100.0	363	12	US-10-205-890-590
7	1858	100.0	363	12	US-10-208-024-590
8	1858	100.0	363	12	US-10-174-581-590
9	1858	100.0	363	12	US-10-176-483-590
10	1858	100.0	363	12	US-10-176-749-590
11	1858	100.0	363	12	US-10-176-914-590
12	1858	100.0	363	12	US-10-176-915-590
13	1858	100.0	363	12	US-10-176-484-590
14	1858	100.0	363	12	US-10-180-550-590
15	1858	100.0	363	12	US-10-180-550-590

16	1858	100.0	363	12	US-10-183-014-590	Sequence 590, App
17	1858	100.0	363	12	US-10-187-738-590	Sequence 590, App
18	1858	100.0	363	12	US-10-187-740-590	Sequence 590, App
19	1858	100.0	363	12	US-10-187-883-590	Sequence 590, App
20	1858	100.0	363	12	US-10-194-363-590	Sequence 590, App
21	1858	100.0	363	12	US-10-194-460-590	Sequence 590, App
22	1858	100.0	363	12	US-10-194-463-590	Sequence 590, App
23	1858	100.0	363	12	US-10-194-484-590	Sequence 590, App
24	1858	100.0	363	12	US-10-195-884-590	Sequence 590, App
25	1858	100.0	363	12	US-10-195-896-590	Sequence 590, App
26	1858	100.0	363	12	US-10-196-744-590	Sequence 590, App
27	1858	100.0	363	12	US-10-196-755-590	Sequence 590, App
28	1858	100.0	363	12	US-10-197-704-590	Sequence 590, App
29	1858	100.0	363	12	US-10-197-710-590	Sequence 590, App
30	1858	100.0	363	12	US-10-198-758-590	Sequence 590, App
31	1858	100.0	363	12	US-10-198-766-590	Sequence 590, App
32	1858	100.0	363	12	US-10-199-304-590	Sequence 590, App
33	1858	100.0	363	12	US-10-199-309-590	Sequence 590, App
34	1858	100.0	363	12	US-10-199-313-590	Sequence 590, App
35	1858	100.0	363	12	US-10-199-456-590	Sequence 590, App
36	1858	100.0	363	12	US-10-201-329-590	Sequence 590, App
37	1858	100.0	363	12	US-10-202-412-590	Sequence 590, App
38	1858	100.0	363	12	US-10-206-919-590	Sequence 590, App
39	1858	100.0	363	12	US-10-206-922-590	Sequence 590, App
40	1858	100.0	363	12	US-10-206-924-590	Sequence 590, App
41	1858	100.0	363	12	US-10-207-914-590	Sequence 590, App
42	1858	100.0	363	12	US-10-207-921-590	Sequence 590, App
43	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App
44	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App
45	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App

ALIGNMENTS

RESULT 1

US-09-736-131-2
; Sequence 2, Application US/09736131
; Patent No. US20020019347A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000738
; CURRENT APPLICATION NUMBER: US/09/736,131
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/219,449
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Human
US-09-736-131-2

Query Match	100.0%	Score 1858;	DB 9;	Length 363;
Best Local Similarity	100.0%	Pred. No. 2.4e-169;		
Matches 363;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRAGVLLVNLGLHLLAALDM	60	
Db	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRAGVLLVNLGLHLLAALDM	60	
QY	61	PTTLGWVRGTPSAGACQVIGFLDTFLASNAALSVAAASADQWLAVGFFLYAGRLRP	120	
Db	61	PTTLGWVRGTPSAGACQVIGFLDTFLASNAALSVAAASADQWLAVGFFLYAGRLRP	120	
QY	121	RYAGLLGCAGQSLAFSGAALGCSWLGYSAFASCSLRPPPRPFAATLHAYG	180	
Db	121	RYAGLLGCAGQSLAFSGAALGCSWLGYSAFASCSLRPPPRPFAATLHAYG	180	

QY 181 FVLPLAVLCITSLQVHRVARRHCQMDTVMKALALLADLHPSVRQRCCLIOKKRRHRAT 240
DB 181 FVLPLAVLCITSLQVHRVARRHCQMDTVMKALALLADLHPSVRQRCCLIOKKRRHRAT 240
QY 241 RKIGIAIAFLICFAPYVMTLAEVLVFFVTVAQWGLSKCLITYSKAVADPFTYSLLRRP 300
DB 241 RKIGIAIAFLICFAPYVMTLAEVLVFFVTVAQWGLSKCLITYSKAVADPFTYSLLRRP 300
QY 301 FRQVLAGMVRHLKRTPRPASTHSDSLDVAGMVHQLLKTTPRPASTHNGSVDTENDSCIQ 360
DB 301 FRQVLAGMVRHLKRTPRPASTHSDSLDVAGMVHQLLKTTPRPASTHNGSVDTENDSCIQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 2
US-09-782-974C-186
; Sequence 186, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPERM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-186

Query Match 100.0%; Score 1858; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEALLAGLVVMTLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPEALLAGLVVMTLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
QY 61 PFTLLGVMGRGTSAPGACQVIGFLDTFLASNALSVALLSADQWLAVGFFPLRYAGRLRP 120
DB 61 PFTLLGVMGRGTSAPGACQVIGFLDTFLASNALSVALLSADQWLAVGFFPLRYAGRLRP 120
QY 121 RYAGLLGCAGWGLAFSGAALGCSWLGYSSAFASCSLRLPPEPRPFAATLHVG 180

DB 121 RYAGLLGCAGWGLAFSGAALGCSWLGYSSAFASCSLRLPPEPRPFAATLHVG 180
QY 181 FVLPLAVLCITSLQVHRVARRHCQMDTVMKALALLADLHPSVRQRCCLIOKKRRHRAT 240
DB 181 FVLPLAVLCITSLQVHRVARRHCQMDTVMKALALLADLHPSVRQRCCLIOKKRRHRAT 240
QY 241 RKIGIAIAFLICFAPYVMTLAEVLVFFVTVAQWGLSKCLITYSKAVADPFTYSLLRRP 300
DB 241 RKIGIAIAFLICFAPYVMTLAEVLVFFVTVAQWGLSKCLITYSKAVADPFTYSLLRRP 300
QY 301 FRQVLAGMVRHLKRTPRPASTHSDSLDVAGMVHQLLKTTPRPASTHNGSVDTENDSCIQ 360
DB 301 FRQVLAGMVRHLKRTPRPASTHSDSLDVAGMVHQLLKTTPRPASTHNGSVDTENDSCIQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 3
US-10-206-915-590
; Sequence 590, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P343ORIC513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 590
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEALLAGLVVMTLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60

Db 1 MGPEALLAGLVNVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPPLRYAGRLRP 120
Db 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPPLRYAGRLRP 120
QY 121 RVAGLLGCGAWGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG 180
Db 121 RVAGLLGCGAWGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG 180
QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 240
Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
Db 241 RKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 360
Db 301 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 360
QY 361 QTH 363
Db 361 QTH 363

RESULT 4
US-10-199-670-590
; Sequence 590, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/10/199,670
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/053266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 590
; LENGTH: 363

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-670-590
Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPEALLAGLVNVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
Db 1 MGPEALLAGLVNVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPPLRYAGRLRP 120
Db 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPPLRYAGRLRP 120
QY 121 RVAGLLGCGAWGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG 180
Db 121 RVAGLLGCGAWGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG 180
QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 240
Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
Db 241 RKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 360
Db 301 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQCLIQOKRRHRAT 360
QY 361 QTH 363
Db 361 QTH 363

RESULT 5
US-10-201-858-590
; Sequence 590, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540

FILE REFERENCE: P3430R1C538
CURRENT APPLICATION NUMBER: US/10/208,024
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 590
LENGTH: 363
TYPE: PRT
ORGANISM: Homo Sapien
US-10-208-024-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169; Indels 0; Gaps 0;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSALRTRASGVLLVNLISLGHLLAALDM	60
Db	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSALRTRASGVLLVNLISLGHLLAALDM	60
QY	61	PFTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP	120
Db	61	PFTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP	120
QY	121	RYAGLLGCWAGQSALFSGAALGCSWLGYSAPASCSLRPPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLGCWAGQSALFSGAALGCSWLGYSAPASCSLRPPPEPRPFAAFTATLHVG	180
QY	181	FVLPLAVLCLTSLQVHRVARRHQCRMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
Db	181	FVLPLAVLCLTSLQVHRVARRHQCRMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
QY	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
QY	301	PROVLAGMVHRLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ	360
Db	301	PROVLAGMVHRLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ	360
QY	361	QTH 363	
Db	361	QTH 363	

RESULT 8

US-10-201-853-590
Sequence 590, Application US/10201853
Publication No. US2004005358A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C465
CURRENT APPLICATION NUMBER: US/10/201,853
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 590
LENGTH: 363
TYPE: PRT
ORGANISM: Homo Sapien
US-10-201-853-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169; Indels 0; Gaps 0;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSALRTRASGVLLVNLISLGHLLAALDM	60
Db	1	MGPGALLAGLLVMVLAVALLSNALVLLCCAYSALRTRASGVLLVNLISLGHLLAALDM	60
QY	61	PFTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP	120
Db	61	PFTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP	120
QY	121	RYAGLLGCWAGQSALFSGAALGCSWLGYSAPASCSLRPPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLGCWAGQSALFSGAALGCSWLGYSAPASCSLRPPPEPRPFAAFTATLHVG	180
QY	181	FVLPLAVLCLTSLQVHRVARRHQCRMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
Db	181	FVLPLAVLCLTSLQVHRVARRHQCRMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
QY	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
QY	301	PROVLAGMVHRLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ	360
Db	301	PROVLAGMVHRLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ	360
QY	361	QTH 363	
Db	361	QTH 363	

RESULT 9
US-10-174-581-590
; Sequence 590 Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088722
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088740
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088811
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPGALLAGLVAVALLSNALVLLCCAYSAELRTRASGVLLVNLVSLGHLILAALDM 60
Db 1 MGPGALLAGLVAVALLSNALVLLCCAYSAELRTRASGVLLVNLVSLGHLILAALDM 60

Qy 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120
Db 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120

Qy 121 RYAGLLGCAWGOSLAFSGAALGCCWLGYSAPASCSRLPPEPRPFAAFTATLHVG 180
Db 121 RYAGLLGCAWGOSLAFSGAALGCCWLGYSAPASCSRLPPEPRPFAAFTATLHVG 180

Qy 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVROKCLIQKRRHRAT 240
Db 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVROKCLIQKRRHRAT 240

Qy 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLRRP 300
Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLRRP 300

Qy 301 PROVLAGMVRHLKRTPRPASTHDSISLDVAGVMVHQLLKRTPRPASTHNGSVDTENDSCLQ 360
Db 301 PROVLAGMVRHLKRTPRPASTHDSISLDVAGVMVHQLLKRTPRPASTHNGSVDTENDSCLQ 360

Qy 361 QTH 363
Db 361 QTH 363

RESULT 10
US-10-176-483-590
; Sequence 590, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1G68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; SEQ ID NO 590
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPGALLAGLVAVALLSNALVLLCCAYSAELRTRASGVLLVNLVSLGHLILAALDM 60
Db 1 MGPGALLAGLVAVALLSNALVLLCCAYSAELRTRASGVLLVNLVSLGHLILAALDM 60

Qy 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120
Db 61 PFTLLGVMGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120

Qy 121 RYAGLLGCAWGOSLAFSGAALGCCWLGYSAPASCSRLPPEPRPFAAFTATLHVG 180
Db 121 RYAGLLGCAWGOSLAFSGAALGCCWLGYSAPASCSRLPPEPRPFAAFTATLHVG 180

Qy 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVROKCLIQKRRHRAT 240
Db 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVROKCLIQKRRHRAT 240

Qy 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLRRP 300
Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLRRP 300

Qy 301 PROVLAGMVRHLKRTPRPASTHDSISLDVAGVMVHQLLKRTPRPASTHNGSVDTENDSCLQ 360
Db 301 PROVLAGMVRHLKRTPRPASTHDSISLDVAGVMVHQLLKRTPRPASTHNGSVDTENDSCLQ 360

QY 361 QTH 363
 Db 361 QTH 363

RESULT 11

US-10-176-749-590

; Sequence 590, Application US/10176749
 ; Publication No. US20030017542A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C76

; CURRENT APPLICATION NUMBER: US/10/176,749

; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 590

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-749-590

Query Match 100.0%; Score 1858; DB 12; Length 363;

Best Local Similarity 100.0%; Pred. No. 2.4e-169;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

Db 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

QY 61 PFTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

Db 61 PFTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

QY 121 RVAGLLGCWAGQSLAFSGAALGCSWLGYSFAFASCSRLRPPPEPRPFAAFTATLHVG 180

Db 121 RVAGLLGCWAGQSLAFSGAALGCSWLGYSFAFASCSRLRPPPEPRPFAAFTATLHVG 180

QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

QY 301 FROVLAGMVRHLIKRTPRPASTHSDSSLDVAGMVHQLKXETPRPASTHNGSVDTENDSCIQ 360

Db 301 FROVLAGMVRHLIKRTPRPASTHSDSSLDVAGMVHQLKXETPRPASTHNGSVDTENDSCIQ 360

QY 361 QTH 363

Db 361 QTH 363

RESULT 12

US-10-176-914-590

; Sequence 590, Application US/10176914

; Publication No. US20030017543A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C83
 ; CURRENT APPLICATION NUMBER: US/10/176,914
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 590
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-914-590

Query Match 100.0%; Score 1858; DB 12; Length 363;

Best Local Similarity 100.0%; Pred. No. 2.4e-169;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

Db 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

QY 61 PFTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

Db 61 PFTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

QY 121 RVAGLLGCWAGQSLAFSGAALGCSWLGYSFAFASCSRLRPPPEPRPFAAFTATLHVG 180

Db 121 RVAGLLGCWAGQSLAFSGAALGCSWLGYSFAFASCSRLRPPPEPRPFAAFTATLHVG 180

QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

QY 301 FROVLAGMVRHLIKRTPRPASTHSDSSLDVAGMVHQLKXETPRPASTHNGSVDTENDSCIQ 360

Db 301 FROVLAGMVRHLIKRTPRPASTHSDSSLDVAGMVHQLKXETPRPASTHNGSVDTENDSCIQ 360

QY 361 QTH 363

Db 361 QTH 363

RESULT 13

US-10-176-915-590

; Sequence 590, Application US/10176915

; Publication No. US20030017544A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C110
/ CURRENT APPLICATION NUMBER: US/10/176,915
/ CURRENT FILING DATE: 2002-06-21
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-915-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSDQWLAVGFPFLRYAGRLRP 120
DB 61 PPTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSDQWLAVGFPFLRYAGRLRP 120
QY 121 RVAGLLGCAGWQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
DB 121 RVAGLLGCAGWQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
QY 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT 240
DB 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTRLAELVFFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
DB 241 RKIGIAIATFLICFAPYVMTRLAELVFFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FRQVLGVMHRLKRTPRPASTHDSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ 360
DB 301 FRQVLGVMHRLKRTPRPASTHDSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 14
US-10-176-484-590
/ Sequence 590, Application US/10176484
/ Publication No. US2003059876A9
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C64
/ CURRENT APPLICATION NUMBER: US/10/176,484
/ CURRENT FILING DATE: 2002-06-20
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien

US-10-176-484-590
Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSDQWLAVGFPFLRYAGRLRP 120
DB 61 PPTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSDQWLAVGFPFLRYAGRLRP 120
QY 121 RVAGLLGCAGWQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
DB 121 RVAGLLGCAGWQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
QY 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT 240
DB 181 FVLPLAVCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTRLAELVFFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
DB 241 RKIGIAIATFLICFAPYVMTRLAELVFFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FRQVLGVMHRLKRTPRPASTHDSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ 360
DB 301 FRQVLGVMHRLKRTPRPASTHDSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCIQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 15
US-10-180-550-590
/ Sequence 590, Application US/10180550
/ Publication No. US2003006440A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C149
/ CURRENT APPLICATION NUMBER: US/10/180,550
/ CURRENT FILING DATE: 2002-06-25
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-180-550-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVMRGRTSPAGACQVIGFLDTFLASNAALSVAAALSDQWLAVGFPFLRYAGRLRP 120

Tue May 18 14:14:52 2004

Db	61	PFTLLGVMGRTPSAPGACQVIGFIDTFLASNAALSVAALSAQWLAVGPFPLRYAGRLRP	120
Qy	121	RYAGLLIGCAGOSLAFSGALGCSWLGYSAPASCSRLPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLIGCAGOSLAFSGALGCSWLGYSAPASCSRLPPEPRPFAAFTATLHVG	180
Qy	181	FVLPLAVLCLTSLQVHRVARRHCOQMDVTVMKALALADLHPSVQRCLIQQKRRHRAT	240
Db	181	FVLPLAVLCLTSLQVHRVARRHCOQMDVTVMKALALADLHPSVQRCLIQQKRRHRAT	240
Qy	241	RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQWGLSKCLTYSKAVADPFTYSLLRRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQWGLSKCLTYSKAVADPFTYSLLRRP	300
Qy	301	PROVLAGVHRLKRTPRPASTHDSLDVAGMVHQLIKRTPRPASTHNGSVDTENDSCLQ	360
Db	301	PROVLAGVHRLKRTPRPASTHDSLDVAGMVHQLIKRTPRPASTHNGSVDTENDSCLQ	360
Qy	361	QTH 363	
Db	361	QTH 363	

Search completed: May 18, 2004, 12:14:05
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:04:02 ; Search time 20 seconds
(without alignments)
1745.876 Million cell updates/sec

Title: US-10-049-569-2

Perfect score: 1858

Sequence: 1 MGPEALLAGLVNVLAVALL.....ASTHNGSVDTENDSCLQPTH 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	13.3	437	2 157942	5-hydroxytryptamin
2	244.5	13.2	440	2 JC5520	serotonin receptor
3	243.5	13.1	388	2 JN0605	somatostatin recep
4	239	12.9	436	2 JN0591	serotonin receptor
5	232.5	12.5	359	2 JC4120	histamine H2 recep
6	231.5	12.5	364	2 JN0763	somatostatin recep
7	231	12.4	363	2 157955	somatostatin recep
8	230.5	12.4	408	1 QRHUBB	beta-3-adrenergic
9	230.5	12.4	414	1 QRHUB3	beta-3-adrenergic
10	229.5	12.4	418	2 G02953	somatostatin recep
11	228.5	12.3	363	2 157940	somatostatin recep
12	228.5	12.3	391	2 A41795	somatostatin recep
13	228.5	12.3	391	2 C41795	somatostatin recep
14	228.5	12.3	391	2 A39297	somatostatin recep
15	228.5	12.3	477	1 DJHDS5	dopamine receptor
16	228	12.3	387	2 JC5949	galanin receptor 2
17	228	12.3	475	2 A41271	dopamine receptor
18	226.5	12.2	420	2 T25689	hypothetical prote
19	224	12.1	457	2 151660	dopamine H2 recep
20	223.5	12.0	359	2 A39008	histamine H2 recep
21	223	12.0	369	2 B41795	somatostatin recep
22	223	12.0	445	2 A48881	serotonin receptor
23	222.5	12.0	384	2 A47249	brain-specific som
24	222	11.9	369	2 A45291	somatostatin recep
25	222	11.9	448	2 A47519	serotonin receptor
26	222	11.9	459	2 A56849	dopamine receptor
27	221	11.9	369	2 JC2083	somatostatin recep
28	220	11.8	359	2 JH0449	histamine H2 recep
29	220	11.8	370	2 148231	serotonin receptor

30 220 11.8 477 2 S71323 alpha-1A adrenergic
31 219 11.8 564 2 A38271 serotonin receptor
32 216 11.8 387 1 DYHDA4 dopamine receptor
33 216 11.6 448 2 S36402 serotonin receptor
34 216 11.6 560 2 A38731 alpha-1A adrenergic
35 215.5 11.6 358 2 JQ1278 histamine H2 recep
36 215 11.6 387 2 S55550 5-HT4S receptor -
37 215 11.6 451 2 I51659 dopamine D1A recep
38 214.5 11.5 444 2 C55986 dopamine receptor
39 214 11.5 418 2 A46226 somatostatin recep
40 213.5 11.5 400 2 S32804 beta-3-adrenergic
41 213 11.5 369 2 D41795 somatostatin recep
42 212.5 11.4 363 2 I50475 dopamine D1 recep
43 212 11.4 406 2 S55349 serotonin 4 recep
44 212 11.4 428 2 S30508 probable G protein
45 212 11.4 487 1 DYRTD1 dopamine receptor

ALIGNMENTS

RESULT 1

157942

S-hydroxytryptamine receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: 157942

R:Monima, F.J.

Mol. Pharmacol. 43, 320-327, 1993

A:Title: Cloning and expression of a novel serotonin receptor with high affinity for tri-

A:Reference number: 157942; PMID:7680751

A:Accession: 157942

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-437 <RES>

A:Cross-references: GB:I03202; NID:G294507; PIDN:AAA40618.1; PID:G294508

C:Superfamily: vertebrate rhodopsin

Query Match 13.3%; Score 248; DB 2; Length 437;

Best Local Similarity 25.3%; Pred. No. 3.3e-13;

Matches 93; Conservative 63; Mismatches 166; Indels 46; Gaps 12;

QY 2 GPGEA-----LLAGLVNVLAVALLSNVALLCCAYSALRTRASGVLLVNLGLHL 53
DB 16 GPGEPPAPGGSGWVAALCVIVLTAAANSLIVLICTQPAVRNT--SNFFLVSTSDL 73
QY 54 LLAALDMPFTLLGVMGRTPSPAGCAQVIGFIDTFLASNAALSVAALSADQWLAVGFPLR 113
DB 74 MVGLVMPAPMLNLYGRWVLARGLCLLTAFDVMCCSASILNLCILSLDRYLLILSPLR 133
QY 114 YAGEL-RPRYAGLLGCANGQSIA----FSGAALGCSWLGYSSAFASCSLRLLPSPERPR 168
DB 134 YKURMTAPRALATLG-AW--SLAALASFLPLLGLWHELGKART-----PAGQCR 181
QY 169 FAA---FTATLHVGFLPLAVLCLTSLQVHRVARHRCQMDTDT-----MKALALIA 218
DB 182 LLASLPVLVASGVTFPLPSGAICFTYCRILLAAKQAVQVASLTGTGAQALETLQVPR 241
QY 219 DLPSVR-----QRCLTQOKRRHRRTKIGIALIFLFCFAPYVMTRLAELVFFVTVNAQ 274
DB 242 TPRPGMESADSRRLATYKSKALKASLTGLIGLGMFFVTLFFVFWNTAAQAQVCCDISPL 301
QY 275 WGIISKCLTYKSAVADPFTYSLRRRFRFQVLGAWVHRLKRTFRPASTHSDSLDVAGMVH 334
DB 302 FDVLT-WLGYCNSMTNPIYPLFMDFKRALG----RFLHASTVPRSTGQCPLPLHVDLS 356
QY 335 QLKRTPR 342
DB 357 QRCOTRQP 364

RESULT 2

JC5520

A;Accession: JN0605
A;Molecule type: DNA
A;Residues: 1-388 <XUY>
A;Cross-references: GB:L14856; NID:G292499; PIDN:AAA36623.1; PID:G292500
R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.;
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of a fourth
A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0762
A;Molecule type: DNA
A;Residues: 1-388 <XAM>
A;Cross-references: GB:D16826; NID:G639907; PIDN:BAA04106.1; PID:G639908
R;Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A;Title: Cloning and characterization of a fourth human somatostatin receptor.
A;Reference number: A47457; MUID:93248256; PMID:8493934
A;Accession: A47457
A;Molecule type: DNA
A;Residues: 1-82, 'V', 84-364, 'K', 366-388 <ROH>
A;Cross-references: GB:L07893; NID:G307429; PIDN:AAA60565.1; PID:G307430
A;Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIPI:130858)
C;Comment: This protein mediates the diverse actions of the tetradecapide somatostatin.
C;Genetics:
A;Gene: GDB:SSVTR4
A;Cross-references: GDB:202662; OMIM:182454
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; photoreceptor; rhodopsin
F;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM2>
F;121-142/Domain: transmembrane #status predicted <TM3>
F;162-184/Domain: transmembrane #status predicted <TM4>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;291-314/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbonylate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted

	Query Match	13.1%	Score 243.5	DB 2	Length 388
	Best Local Similarity	25.5%	Pred. No. 6.9e-13		
	Matches	84	Conservative	55	Mismatches 124; Indels 67; Gaps 10;
QY	2	GPGEALLAGLL-----VMVLAVALLNALVLLCCAYSALRTRASGVLLVNLGLHLL	55		
Db	38	GPGDARAAGVAIQCIYALVCLGLVGNALVIFVILRYAKMKT-ATNIIYLINLAVALDEL	96		
QY	56	AALDMPFTLLGVMGRTPSAPGACQVIGFDTFLASNAALSAALSDQWLVGFPLRYA	115		
Db	97	-MLSVFPVASSAALRHPPFGSVLCRAVLSDGLNMFTSVCLTVLSVDRYVAVVHPLRAA	155		
QY	116	GRLEPRYAGLLGCAGQSL-----AFSGAALGCS--WLGYSAPASCCLR	159		
Db	156	TYRRPSVAKLINLGVLASLLVTLPIAFADTRPARGQVACNLOW-----	202		
QY	160	LPPEPERPERFAATLHAGVFLPLAVLCITSLQVHVARRHCOQMDVTVMKALLAD	219		
Db	203	-----PHPNWSAVVVYVYFLGFLPLVLAIGL-----CYLLIVGKRAVALRAG	246		
QY	220	LHPSVQRCLIQCKRRHRRATKIGIAIATFLICFAYVWTRLAELVPFVTVNAQWILS	279		
Db	247	WQ-----QRRSEKKITRLVLMVWVVFVLCWMPFYVYVQLNLV-VTSLDATVNHVS	296		
QY	280	KCLTYSKAVADPFTYSLL---RRPFQVL	305		
Db	297	LILSVANSANPIYGLFSNFRSPQVRL	326		

RESULT 4
JN0591
serotonin receptor 6 - rat

N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HTR6)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999

C:Accession: JN0591

R:Ruut, M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; Schw

Biochem. Biophys. Res. Commun. 193, 268-276, 1993

A:Title: A novel rat serotonin (5-HT₆) receptor: molecular cloning, localization and st

A:Reference number: JN0591; MUID:93277562; PMID:8389146

A:Accession: JN0591

A:Molecule type: DNA

A:Residues: 1-436 <RUA>

A:Cross-references: GB:S62043; NID:G385708; PIDN:AB26908.1; PID:G385709

C:Genetics:

A:Introns: 238/3

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein

F:29-53/Domain: transmembrane #status predicted <TM1>

F:63-84/Domain: transmembrane #status predicted <TM2>

F:95-122/Domain: transmembrane #status predicted <TM3>

F:141-168/Domain: transmembrane #status predicted <TM4>

F:185-213/Domain: transmembrane #status predicted <TM5>

F:267-293/Domain: transmembrane #status predicted <TM6>

F:297-319/Domain: transmembrane #status predicted <TM7>

F:9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 239; DB 2; Length 436;

Best Local Similarity 25.7%; Pred. No. 1.9e-12;

Matches 65; Conservative 58; Mismatches 146; Indels 42; Gaps 11;

QY 2 GPGEA-----LLAGLLVNLVALLSNALVLLCCAYSAELTRASGVLLNLSLGH 53

DB 16 GPGPPPPAGGGGWAALCVIVITAAANSLIIVLICQPALNT--SNFLVSLFTSL 73

QY 54 LLAALDMPFTLLGVNRGTPAGACOVIGFDLTFASNAALSVAALSADWLAVGFPLR 113

DB 74 MVGLVMPPALNLYGRWLARGLLWTFADVMCCSASILNCLISLDRLYLLISPLR 133

QY 114 YAGRL-RRYAGLLGAWGSLA----FSGALGCSWLGYSAPFASCSRLRPPEPRP 168

DB 134 YKLRWTPRALALIG-AW--SLAALASFLPLGLLGHGKART-----PAPGOCR 181

QY 169 FAA---FTATLHAYGVFLPLAVLCLTSLQVHRVARRHCORMDTVT-----MKALALLA 218

DB 182 LLASLPFLVNLVAGVTFFPLSGAICTYCRILLAAKQAVQASLTGTGAQALETLQVPR 241

QY 219 DLHSVR-----ORCLQOKRRHRATKIGIATATFLICFAPVMTLAEVLPFTVNAQ 274

DB 242 TPRGMSADSRRLATKHSRKALKASUTGLILGMFFVTWLPFFVANIAQAVDCISPLG 301

QY 275 WGIILSKCLITYSKAVADPFTYSLRRPQVLL 305

DB 302 FDLVT-WLGYCNSTWNPILVFLMRDPKRAL 331

RESULT 5

JC4120

C:Species: Cavia porcellus (guinea pig)

C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 24-Nov-1999

C:Accession: JC4120

R:Traiffort, E.; Vizete, M.L.; Tardivel-Lacombe, J.; Souil, E.; Schwartz, J.C.; Ruat, M

Biochem. Biophys. Res. Commun. 211, 570-577, 1995

A:Title: The guinea pig histamine H2 receptor: gene cloning, tissue expression and chrom

A:Reference number: JC4120; MUID:95314628; PMID:7794271

A:Accession: JC4120

A:Molecule type: DNA

A:Residues: 1-359 <TRA>

A:Comment: Histamine, a messenger molecule in cell-to-cell communication, affects its ta

ly defined receptor subtypes named H1, H2 and H3.

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:22-45/Domain: transmembrane #status predicted <TM1>

F:58-81/Domain: transmembrane #status predicted <TM2>

F:93-113/Domain: transmembrane #status predicted <TM3>

F:136-157/Domain: transmembrane #status predicted <TM4>

F:179-236/Domain: transmembrane #status predicted <TM5>

F:235-236/Domain: transmembrane #status predicted <TM6>

F:269-289/Domain: transmembrane #status predicted <TM7>

F:162,168/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:221,316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:226,357/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 12.5%; Score 232.5; DB 2; Length 359;

Best Local Similarity 22.0%; Pred. No. 5.4e-12;

Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;

QY 11 LVMVLAVALLSNALVLLCCAYSAELTRASGVLLNLSLGHLLLAALDMPFTLLGVNRG 70

DB 24 ILIILITVTVAGNVVCLAVGLNRRLRS-LTNCFIYSLAVTDLILLGLLVLPFSAIYQLSC 82

QY 71 RTPSAGCACOVIGFDLTFASNAALSVAALSADWLAVGFPLRYAGRLPRYAGLLGCA 130

DB 83 KWSFSKVPCHYIYTSLDVMLCTASILNLFMSLDRYCAVTDPLRYPVLIITPARVAISLVFI 142

QY 131 WQGLAFSGAALGCSWLGYSAPFASCSRLRPPEPRPFAAFTATLHAYGVFLP 184

DB 143 WVISITLSFLSIHLGWSNRNETSKNDTIYCKVQVN-----EYGLVDGLVTFYLP 194

QY 185 LAVCLTSLQVHRVARRHCORMDTV-TMKALALLADLHPFSVRQCLIQOKRRHRATRKI 243

DB 195 LLIMCIYFRIKAREQARRINHIGSWKAATI-----REHKATVTL 236

QY 244 GIAIATFLICFAPVMTLAEVLPFV-----TVNAWGILSKCLITYSKAVADPFTYS 295

DB 237 AAVNGARFIICFFPY-----FTVFYRGLKGDVAINEVFEDVVLWGLVANSALNPILYA 289

QY 296 LLRRPFOVLGAVHRLKKTTPRPASTHDSLS 327

DB 290 ALNEDFRTA---YHQLFCCRLASHNSHETSLS 317

RESULT 6

JN0763

somatostatin receptor 5 - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000

C:Accession: JN0763

R:Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; Li

Biochem. Biophys. Res. Commun. 195, 844-852, 1993

A:Title: Cloning, functional expression and pharmacological characterization of a fourth

A:Reference number: JN0762; MUID:93384611; PMID:8373420

A:Accession: JN0763

A:Molecule type: DNA

A:Residues: 1-364 <YAM>

A:Cross-references: DDBJ:D16827; NID:G487683; PIDN:BA04107.1; PID:G487684

A:Comment: This protein is a member of somatostatin receptor family.

C:Genetics:

A:Gene: GDB:SSTR5

A:Cross-references: GDB:138452; OMIM:182455

A:Map position: 16p13.3-16p13.3

A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiole

F:40-66/Domain: transmembrane #status predicted <TM1>

F:77-102/Domain: transmembrane #status predicted <TM2>

F:114-135/Domain: transmembrane #status predicted <TM3>

F:155-177/Domain: transmembrane #status predicted <TM4>

F:196-228/Domain: transmembrane #status predicted <TM5>

F:246-273/Domain: transmembrane #status predicted <TM6>

F:280-307/Domain: transmembrane #status predicted <TM7>

F:13, 26, 187/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:112-186/Disulfide bonds: #status predicted

F:242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr

F:247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predict

F:320/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.5%; Score 231.5; DB 2; Length 364;
Best Local Similarity 25.0%; Pred. No. 6.6e-12;
Matches 92; Conservative 51; Mismatches 166; Indels 59; Gaps 11;

QY 2 GPGEALLAGLVVAVALLSNALVLLCCAYSAELRTRASGVLLVNLISGLHLLAALDMP 61
DB 37 GARAVLPVLYLVCAAGLGNTLVIVVLRFAKMT-VTNIILNLAVADVLY-MGLP 94
QY 62 FTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPIRYAGRLRPR 121
DB 95 FLATQNAASFPPFGPVLCLRLVMTLDGNOFTSVFCLTVMSVDRLVAVVHPPLSSARWRPR 154
QY 122 YAGLLGCGAQGLAFS-----GAALGCSMLGYSSAFASCSRLRPPERPFA 170
DB 155 VAKLASAAVNLSCMSLPLLVFADVQEGGTGNASW-----PEPVGLWGA 199
QY 171 APTATLHAGVFLVPLAVLCITLSQVHRVARRHCQMDVTMKALALLADLHPSVRQCLI 230
DB 200 VFIYITAVLGFFAPLVLICL-----CYLLIVVKVRA-----AGVRVGCV- 238
QY 231 QOKRRHRARFKIGIAITFLICFAPV---MTRLAELVPFVTVAQWGLSKCLITYSKA 287
DB 239 -RRSERKVTMVLVVLVFPAGCWLFFFTVINVLAVLPQEPASAGLYFFVWILSYANS 297
QY 288 VADPFTYSLRRPFRQVLAGVHRLKTRPRPASTHSDSLDVAGVHQLLKRT-PRPAST 345
DB 298 CANPVLGYGLSDNFRQSFQKV---LCLRKSGAKADATEPRPDRIROQQEATP-PAHRA 353
QY 346 THNGSVDT 353
DB 354 ANGLMOT 361

RESULT 7
157955
somatostatin receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
X:Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchishyn, L.L.; Day, R.; Niznik, H.B.;
Mol. Pharmacol. 45, 417-427, 1994
A:Title: Molecular cloning, functional characterization, and chromosomal localization of
A:Reference number: 157955; MUID:94195267; PMID:7908405
A:Accession: 157955
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-363 <RES>
A:Cross-references: GB:L14865; NID:9431094; PIDN:AAA0828.1; PID:g431095
C:Genetics:
A:Gene: GDB:SST
A:Map position: 3q28-3q28
C:Superfamily: vertebrate rhodopsin

Query Match 12.4%; Score 231; DB 2; Length 363;
Best Local Similarity 25.1%; Pred. No. 7.2e-12;
Matches 92; Conservative 51; Mismatches 166; Indels 58; Gaps 11;

QY 2 GPGEALLAGLVVAVALLSNALVLLCCAYSAELRTRASGVLLVNLISGLHLLAALDMP 61
DB 37 GARAVLPVLYLVCAAGLGNTLVIVVLRFAKMT-VTNIILNLAVADVLY-MGLP 94
QY 62 FTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFPIRYAGRLRPR 121
DB 95 FLATQNAASFPPFGPVLCLRLVMTLDGNOFTSVFCLTVMSVDRLVAVVHPPLSSARWRPR 154
QY 122 YAGLLGCGAQGLAFS-----GAALGCSMLGYSSAFASCSRLRPPERPFA 170
DB 155 VAKLASAAVNLSCMSLPLLVFADVQEGGTGNASW-----PEPVGLWGA 199
QY 171 APTATLHAGVFLVPLAVLCITLSQVHRVARRHCQMDVTMKALALLADLHPSVRQCLI 230
DB 200 VFIYITAVLGFFAPLVLICL-----CYLLIVVKVRA-----AGVRVGCV- 238

QY 231 QOKRRHRARFKIGIAITFLICFAPV---MTRLAELVPFVTVAQWGLSKCLITYSKA 287
DB 239 -RRSERKVTMVLVVLVFPAGCWLFFFTVINVLAVLPQEPASAGLYFFVWILSYANS 297
QY 288 VADPFTYSLRRPFRQVLAGVHRLKTRPRPASTHSDSLDVAGVHQLLKRT-PRPAST 345
DB 298 CANPVLGYGLSDNFRQSFQKV---LCLRKSGAKADATEPRPDRIROQQEATP-PAHRA 354
QY 347 HNGSVDT 353
DB 355 -NGLMOT 360

RESULT 8
QKUBE
beta-3-adrenergic receptor, splice form 3 - human
N:Alternate names: beta-3-adrenergic receptor form B
N:Contains: beta-3-adrenergic receptor splice form 1
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
X:Leiss, J.M.; Kaghad, M.; Rodriguez, M.; Chalon, P.; Bonnin, J.; Dupre, I.; Delpech, B.;
FEBS Lett. 324, 127-130, 1993
A:Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.
A:Reference number: S33751; MUID:93285320; PMID:8389717
A:Accession: S33751
A:Molecule type: mRNA
A:Residues: 1-408 <LEL1>
A:Cross-references: EMBL:X70811; NID:g312396; PIDN:CAA50141.1; PID:g312397
A:Note: Splice form 3
A:Accession: S33753
A:Molecule type: DNA
A:Residues: 392-408 <LEL2>
A:Cross-references: GB:X70812; NID:g312398; PIDN:CAA50143.1; PID:g1666376
R:Emorine, L.J.
submitted to the EMBL Data Library, March 1993
A:Reference number: S32803
A:Molecule type: DNA
A:Residues: 1-408 <EMO>
A:Cross-references: EMBL:X72861; NID:g98094; PIDN:CAA51383.1; PID:g298095
R:van Spronsen, A.; Nahmias, C.; Krief, S.; Briand-Sutren, M.M.; Strosberg, A.D.; Emorine
Eur. J. Biochem. 213, 1117-1124, 1993
A:Title: The promoter and intron/exon structure of the human and mouse beta3-adrenergic-1
A:Reference number: S32826; MUID:93279311; PMID:8389293
A:Accession: S32826
A:Molecule type: DNA
A:Residues: 1-87344-350;394-408 <SPR>
C:Genetics:
A:Gene: GDB:ADRB3
A:Cross-references: GDB:203869; OMIM:109691
A:Map position: 8p12-8p11.1
A:Introns: 402/2
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:1-408/Product: beta-3-adrenergic receptor precursor splice form 3 #status predicted <W>
F:1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <W>
F:37-63/Domain: transmembrane #status predicted <TM1>
F:73-101/Domain: transmembrane #status predicted <TM2>
F:113-133/Domain: transmembrane #status predicted <TM3>
F:156-178/Domain: transmembrane #status predicted <TM4>
F:204-225/Domain: transmembrane #status predicted <TM5>
F:293-314/Domain: transmembrane #status predicted <TM6>
F:327-347/Domain: transmembrane #status predicted <TM7>
F:8,26/Binding site: carbohydrate (Asn) #status predicted

Query Match 12.4%; Score 230.5; DB 1; Length 408;
Best Local Similarity 24.9%; Pred. No. 9e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

QY 3 PGEALLAGLVVAVALLSNALVLLCCAYSAELRTRASGVLLVNLISGLHLLAAL 58

Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPLQOT-MTNVFTVTSIAAADLVWGLL 89
QY 59 DMPFTLLGVMGRGRTSPAGCAQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVTSIETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAATL 176
Db 150 TKRCARTAVLVVWVSAVSPAPIMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 215
Db 203 PYVLLSSVSFYPLDLVLMVLFVYARVFWATRLRLRGELGFPPEESPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIQKRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 VGTCPPEGVACGRPARLLPLREHRLCTGLGIMGTTCWLFPFLANVLRALGPGSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPQVLAGWVHRLKTRP 319
Db 323 VPGPAFLALN-W-----LGYSANAFNPLIYCRSPDPSAFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLLDVAGM 332
Db 372 CAARPALPFGSV 384
RESULT 9
ORHUB3
beta-3-adrenergic receptor, splice form 2 - human
N;Alternate names: beta-3-adrenergic receptor form A
N;Contains: beta-3-adrenergic receptor splice form 1
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
R;Accession: A41348; S33752
R;Emorine, L.J.; Marullo, S.; Briand-Sutren, M.M.; Patey, G.; Tate, K.; Delavier-Klutch
Science 245, 1118-1121, 1999
A;Title: Molecular characterization of the human beta-3-adrenergic receptor.
A;Reference number: A41348; MUID:89368947; PMID:2570461
A;Status: nucleic acid sequence not shown
A;Accession: A41348
A;Molecule type: DNA
A;Residues: 1-402 <BMO>
A;Cross-references: GB:M29932; NID:G178895; PIDN:AAA35550.1; PID:G178896
A;Note: splice form 1
R;Leilas, J.M.; Kagnad, M.; Rodriguez, M.; Chalon, P.; Bonnin, J.; Dupre, I.; Delpech, E
FEBS Lett. 324, 127-130, 1993
A;Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.
A;Reference number: S33751; MUID:93285320; PMID:8389717
A;Accession: S33752
A;Molecule type: DNA
A;Residues: 392-414 <LEL>
A;Cross-references: EMBL:X70812; NID:G312398; PIDN:CAA50142.1; PID:G1666375
A;Note: splice form 2
C;Genetics:
A;Gene: GDB:ADRB3
A;Cross-references: GDB:203869; OMIM:109691
A;Map position: 8p12-8p11.1
A;Introns: 402/2
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F;1-414/Product: beta-3-adrenergic receptor precursor splice form 2 #status predicted <M
F;1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <M
F;37-63/Domain: transmembrane #status predicted <TM1>
F;73-101/Domain: transmembrane #status predicted <TM2>
F;113-133/Domain: transmembrane #status predicted <TM3>
F;156-178/Domain: transmembrane #status predicted <TM4>
F;204-225/Domain: transmembrane #status predicted <TM5>
F;293-314/Domain: transmembrane #status predicted <TM6>
F;327-347/Domain: transmembrane #status predicted <TM7>
F;8,26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Best Local Similarity 24.9%; Pred. No. 9.2e-12; Mismatches 154; Indels 65; Gaps 14;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVWVLAVALLS-----NALVLLCCAYSALRTRASGVLLVNLGHLILAAL 58
Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPLQOT-MTNVFTVTSIAAADLVWGLL 89
QY 59 DMPFTLLGVMGRGRTSPAGCAQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVTSIETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAATL 176
Db 150 TKRCARTAVLVVWVSAVSPAPIMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 215
Db 203 PYVLLSSVSFYPLDLVLMVLFVYARVFWATRLRLRGELGFPPEESPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIQKRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 VGTCPPEGVACGRPARLLPLREHRLCTGLGIMGTTCWLFPFLANVLRALGPGSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPQVLAGWVHRLKTRP 319
Db 323 VPGPAFLALN-W-----LGYSANAFNPLIYCRSPDPSAFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLLDVAGM 332
Db 372 CAARPALPFGSV 384
RESULT 10
G02953
beta-3-adrenergic receptor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 13-Aug-1999
R;Lowe, A.L.; Walston, J.; Shuldiner, A.R.
submitted to the EMBL Data Library, July 1996
A;Reference number: H01989
A;Accession: G02953
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-418 <LOW>
A;Cross-references: EMBL:U63592; NID:G1458230; PIDN:AAB53939.1; PID:G1458232
C;Genetics:
A;Introns: 402/1
C;Superfamily: vertebrate rhodopsin
Query Match 12.4%; Score 229.5; DB 2; Length 418;
Best Local Similarity 25.9%; Pred. No. 1.1e-11;
Matches 95; Conservative 56; Mismatches 149; Indels 67; Gaps 15;
QY 3 PGEALLAGLLVWVLAVALLS-----NALVLLCCAYSALRTRASGVLLVNLGHLILAAL 58
Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPLQOT-MTNVFTVTSIAAADLVWGLL 89
QY 59 DMPFTLLGVMGRGRTSPAGCAQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVTSIETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAATL 176
Db 150 TKRCARTAVLVVWVSAVSPAPIMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 224
Db 203 PYVLLSSVSFYPLDLVLMVLFVYARVFWATRLRLRGELGFPPEESPAPSRSLAPAP 262
QY 225 RQRCLIQO-----KRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 AGTCAPPEGVACGRPARLLPLREHRLCTGLGIMGTTCWLFPFLANVLRALGPGSL 322

C41795
somatostatin receptor 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C/Accession: C41795
R/Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A/Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
A/Reference number: A41795; MUID:92108031; PMID:1346068
A/Accession: C41795
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-391 <VAM>
A/Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 12.3%; Score 228.5; DB 2; Length 391;
Best Local Similarity 24.5%; Pred. No. 1.3e-11;
Matches 78; Conservative 61; Mismatches 131; Indels 49; Gaps 11;

QY 2 GPEALLAGLLVMVLA-VALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM 60
DB 54 GQSAILISFIYSVCLVGLCGNSMWIYILRYAKMT-ATNIYILNLAIDELL-MLSV 111
QY 61 PFTLLGVNRGRTSPAGCACQVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP 120
DB 112 PFLVTSTLLRHWPFGALLCRVLSDVAVNMFTSIYCLTVLSVDVRYAVVHPKAAARYRP 171
QY 121 RYAGLLGCWAGQSL-----AFSGAALCGSWLGYSSAFASCSRLRPPPERPFAAPT 173
DB 172 TVAKVNLGVWVLSLVILPIVVFSTRAN-----SDGTVACNM-LMPEPAQRWLVGFV 224
QY 174 ATLHAGVFLPLAVLCITSLQVHRVARRHCQMDVTMKALLADLHPSVRQCLIQOK 233
DB 225 LYTFMGFLLPVGAICL-----CYVLIIAKRWVAKAGWQ-----QRK 263
QY 234 RRRHRAIRKIGIAIATFLICFAPYVMTRELAVL---PFTVNAQWGLSKCLTYSKAVD 290
DB 264 RSEKRTILMVMVMVVFICWMPFYVQLVNVAEQDQATVSQ----LSVILGYANSCAN 319
QY 291 PFTYSLL---RRPFRQVL 305
DB 320 PLYGFLSDNFKRSFORIL 338

RESULT 14
A39297
somatostatin receptor - rat
N/Alternate names: probable G-protein-coupled receptor; SRIF receptor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C/Accession: A39297; A45102; S20088
R/Meyerhof, W.; Faust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A/Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed in rat brain
A/Reference number: A39297; MUID:92096119; PMID:1861599
A/Accession: A39297
A/Molecule type: mRNA
A/Residues: 1-391 <MEY>
A/Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
A/Experimental source: brain
A/Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated at Met-2
J. Biol. Chem. 267, 21307-21312, 1992
A/Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A/Reference number: A45102; MUID:93016064; PMID:1400442
A/Accession: A45102
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-391 <LII>
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBIP:116692)

C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 12.3%; Score 228.5; DB 2; Length 391;
Best Local Similarity 24.5%; Pred. No. 1.3e-11;
Matches 78; Conservative 61; Mismatches 131; Indels 49; Gaps 11;

QY 2 GPEALLAGLLVMVLA-VALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM 60
DB 54 GQSAILISFIYSVCLVGLCGNSMWIYILRYAKMT-ATNIYILNLAIDELL-MLSV 111
QY 61 PFTLLGVNRGRTSPAGCACQVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP 120
DB 112 PFLVTSTLLRHWPFGALLCRVLSDVAVNMFTSIYCLTVLSVDVRYAVVHPKAAARYRP 171
QY 121 RYAGLLGCWAGQSL-----AFSGAALCGSWLGYSSAFASCSRLRPPPERPFAAPT 173
DB 172 TVAKVNLGVWVLSLVILPIVVFSTRAN-----SDGTVACNM-LMPEPAQRWLVGFV 224
QY 174 ATLHAGVFLPLAVLCITSLQVHRVARRHCQMDVTMKALLADLHPSVRQCLIQOK 233
DB 225 LYTFMGFLLPVGAICL-----CYVLIIAKRWVAKAGWQ-----QRK 263
QY 234 RRRHRAIRKIGIAIATFLICFAPYVMTRELAVL---PFTVNAQWGLSKCLTYSKAVD 290
DB 264 RSEKRTILMVMVMVVFICWMPFYVQLVNVAEQDQATVSQ----LSVILGYANSCAN 319
QY 291 PFTYSLL---RRPFRQVL 305
DB 320 PLYGFLSDNFKRSFORIL 338

RESULT 15
DYNHDS
dopamine receptor D5 - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C/Accession: S15080; A41232
R/Sunahara, R.K.; Guan, H.C.; O'Dowd, B.F.; Seeman, P.; Laurant, L.G.; Ng, G.; George, S.
Nature 350, 614-619, 1991
A/Title: Cloning of the gene for a human dopamine D(5) receptor with higher affinity for dopamine
A/Reference number: S15080; MUID:91204055; PMID:1826762
A/Accession: S15080
A/Molecule type: DNA
A/Residues: 1-477 <SUN>
A/Cross-references: EMBL:X58454; NID:g32048; PIDN:CAA1360.1; PID:g32049
R/Grandy, D.K.; Zhang, Y.; Bouvier, C.; Zhou, Q.Y.; Johnson, R.A.; Allen, L.; Buck, K.; F.
Proc. Natl. Acad. Sci. U.S.A. 88, 9175-9179, 1991
A/Title: Multiple human D-5 dopamine receptor genes: a functional receptor and two pseudogenes
A/Reference number: A41232; MUID:92021013; PMID:1833775
A/Accession: A41232
A/Molecule type: DNA
A/Residues: 1-477 <GRA>
A/Cross-references: GB:M67439; NID:g181830; PIDN:AAA52329.1; PID:g181831
C/Genetics:
A/Gene: GDB:DRD5; DRD12
A/Cross-references: GDB:127548; OMIM:126453
A/Map position: 4p15.3-4p15.1
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter receptor
F.78-104/Domain: transmembrane #status predicted <TM1>
F.115-136/Domain: transmembrane #status predicted <TM3>
F.157-180/Domain: transmembrane #status predicted <TM4>
F.225-245/Domain: transmembrane #status predicted <TM5>
F.246-237/Domain: intracellular #status predicted <INT>
F.298-319/Domain: transmembrane #status predicted <TM6>
F.341-361/Domain: transmembrane #status predicted <TM7>
F.7.199/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.113-217/Disulfide bonds: #status predicted
F.153,252/Binding site: phosphate (Thr) (covalent) #status predicted
F.260,271,283/Binding site: phosphate (Ser) (covalent) #status predicted
F.375/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.3%; Score 228.5; DB 1; Length 477;
Best Local Similarity 21.6%; Pred. No. 1.6e-11;
Matches 90; Conservative 82; Mismatches 162; Indels 83; Gaps 17;

Qy	1	MGPGELLGLLVMLVALLSNALVLLCCAYSABLRTASGVLLVNLGLHLLAALDM	60
Db	36	LGPSQVVTACILLTLIIITLLGNVLVCAAIVRSHLRANNTNFIIVSLAVSDLFVALLVM	95
Qy	61	PFTLLGVNRGRTSPAGA-COVIGFLDTFLASNAALSVAALSDQWLAVGFFPLRYAGRLR	119
Db	96	PKKAVAEVAGYWPFF-GAFCDVWVAFDIMCSTASILNLCVISVDRYWAISEPPRYKRYWT	153
Qy	120	PRYAGLLGCGAGSLAFSGAALGCSWLGYSAPASCSLRLLPP-----EPE-	165
Db	154	QRMALVMVGLAWTLTSLIISFTIPVQLNW-HRDQASWGGLDLPNNLANWTPEEDFWEPDV	212
Qy	166	-----RPFPAFTATLHAGVFLPLAVLCLTSLOVHRVARRHCOORMDTVTMKA----	213
Db	213	NAENCDSLNRYAISSL--ISFYIPVAINIVTYIRIAQVQIRISSLERAEHAQ	270
Qy	214	-LALLADLHPSVRQRCILQOKRRHRATRKIGIAIATFLICFAPYVMTRLAELVPPFTVN	272
Db	271	SCRSSAACAPDTSLRASI---KKTETKVLKTLSTVMGVGCWLPFFI--LNCMVPPFCSGH	325
Qy	273	AQ-----WGILSKCLTYSKAVADPFTYSL---LRPFRQVLAGMVHR	311
Db	326	PEGPPAGFPVCVSETTFDFVW-----FGWANSLSNPVIYAFNADFOKFAQLL-GCSH-	377
Qy	312	LLKETPRPASTHDSLL-----DV-----AGMVHQLLKETPRPASTHNGSVDTEND	356
Db	378	FCSRTPTVETVNISNELISYNQDIVFKHEIAAAAYTHW----PNAVTPGNREVDNDEE	430

Search completed: May 18, 2004, 12:08:40
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:01:36 ; Search time 18 Seconds
(without alignments)
1050.081 Million cell updates/sec

Title: US-10-049-569-2
Perfect score: 1858
Sequence: 1 MGFALLAGLVWVLAVAL.....ASTNGSVDTENDSLQOOTH 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1843	99.2	363	1 GP78 HUMAN	Q96P69 homo sapien
2	848	45.6	337	1 GP26 HUMAN	Q8ndv2 homo sapien
3	823	44.3	337	1 GP26 RAT	Q9bx13 rattus norv
4	822	44.2	337	1 GP26 MOUSE	Q8bza7 mus musculu
5	245.5	13.2	440	1 SH6 MOUSE	Q9xl1c8 mus musculu
6	244.5	13.2	440	1 SH6 HUMAN	P50406 homo sapien
7	243.5	13.1	388	1 SH4 HUMAN	P31391 homo sapien
8	239	12.9	436	1 SH6 RAT	P31388 rattus norv
9	232.5	12.5	359	1 HH2R CAVPO	P47747 cavia porce
10	232	12.5	388	1 SH4 MOUSE	P97288 mus musculu
11	231.5	12.5	364	1 SSR5 HUMAN	P35346 homo sapien
12	230.5	12.4	408	1 B3AR HUMAN	P13945 homo sapien
13	229.5	12.4	418	1 B3AR MACMU	Q28524 macaca mula
14	229.5	12.4	425	1 OX1R HUMAN	O43613 homo sapien
15	229	12.3	362	1 SSR5 MOUSE	O08858 mus musculu
16	228.5	12.3	363	1 SSR5 RAT	P30938 rattus norv
17	228.5	12.3	391	1 SSR1 HUMAN	P30872 homo sapien
18	228.5	12.3	391	1 SSR1 MOUSE	P30873 mus musculu
19	228.5	12.3	391	1 SSR1 RAT	P28646 rattus norv
20	228.5	12.3	477	1 DBDR HUMAN	P21918 homo sapien
21	228	12.3	387	1 DBDR HUMAN	O43603 homo sapien
22	228	12.3	475	1 DBDR RAT	P25115 rattus norv
23	224.5	12.1	358	1 HH2R MOUSE	P97292 mus musculu
24	224	12.1	372	1 GAL5 RAT	O08726 rattus norv
25	224	12.1	457	1 DBDR XENLA	P42290 xenopus lae
26	224	12.1	514	1 A1AB MOUSE	P97717 mus musculu
27	223.5	12.0	359	1 HH2R CANFA	P17124 canis famil
28	223	12.0	369	1 SSR2 HUMAN	P30874 homo sapien
29	223	12.0	388	1 SH4 CAVPO	O70528 cavia porce
30	223	12.0	467	1 B1AF BOVIN	Q9ct96 bos taurus
31	223	12.0	479	1 SH7 HUMAN	P34969 homo sapien
32	222.5	12.0	384	1 SSR4 RAT	P30937 rattus norv
33	222.5	12.0	561	1 A1AD RAT	P23944 rattus norv

ALIGNMENTS

RESULT 1			
GP78	HUMAN	STANDARD;	PRT; 363 AA.
ID	Q96P69; Q8NGV3;		
AC	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Probable G protein-coupled receptor GPR78.		
GN	GPR78.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21458557; PubMed=11574155;		
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,		
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;		
RT	"Discovery and mapping of ten novel G protein-coupled receptor		
RT	genes.";		
RL	Gene 275:83-91(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,		
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;		
RT	"Genome-wide discovery and analysis of human seven transmembrane helix		
RT	receptor genes.";		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	INDUCTION.		
RX	MEDLINE=20175424; PubMed=10708769;		
RA	van Laar T., Schouten T., Hoogerwerf E., van Eck M., van der Eb A.J.,		
RA	Terleth C.;		
RT	"The novel WMS-inducible gene Mif1/KIAA0025 is a target of the		
RT	unfolded protein response pathway.";		
RL	FEBS Lett. 469:123-131(2000).		
CC	-1- FUNCTION: Orphan receptor.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: Expressed in pituitary and placenta. No		
CC	expression detected in brain, skeletal muscle, lung, heart, liver,		
CC	pancreas, or kidney.		
CC	-1- INDUCTION: Expression increased in fibroblasts or HeLa cells		
CC	following UV-A irradiation, exposure to DNA-alkylating agents, or		
CC	endoplasmic reticulum (ER) stress caused by osmotic shock or the		
CC	glycosylation inhibitor tunicamycin.		
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF411107; AAL26479.1; -.		

P30680 rattus norv
Q13639 homo sapien
P32305 rattus norv
P53452 fugu rubrip
O88854 mus musculu
P34994 sus scrofa
P25021 homo sapien
P50021 pan troglod
P31387 mus musculu
Q91175 oryzias lat
P97714 mus musculu
O02662 canis famil

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DR EMBL; AB065673; BAC05898.1; -.
DR Genew; HGNC:4528; GPR78.
DR MIM; 606921; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 7
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 8 28
FT DOMAIN 29 47
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68
FT DOMAIN 69 80
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 81 101
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 102 122
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 123 143
FT DOMAIN 144 168
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 169 189
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 190 242
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 263
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 264 277
FT TRANSMEM 278 297
FT TRANSMEM 298 363
FT DISULFID 79 156
FT CONFLICT 216 216
FT CONFLICT 226 227
FT CONFLICT HG -> L (IN REF. 2).
SQ SEQUENCE 363 AA; 39228 MW; 00B6D9F7E768E0ED CRC64;

Query Match 99.2%; Score 1843; DB 1; Length 363;
Best Local Similarity 99.2%; Pred. No. 4.4e-130;
Matches 360; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
QY 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120
DB 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120
QY 121 RVAGLLGCAGQSLAFSGAALGCSWLGYSYSAFASCSLRLPPEPRPFAATLHVG 180
DB 121 RVAGLLGCAGQSLAFSGAALGCSWLGYSYSAFASCSLRLPPEPRPFAATLHVG 180
QY 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCQLQKRRHRAT 240
DB 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCQLQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVNTLAEVLVPEVTYNAQNGILSKCLTYSKAVADPFTVSLRLRP 300
DB 241 RKIGIAIATFLICFAPYVNTLAEVLVPEVTYNAQNGILSKCLTYSKAVADPFTVSLRLRP 300
QY 301 FRQVLAVGVRHLLKRTPRPASTHSSLDVAGVHQLKRTPRPASTHNGSVDTENDSCLQ 360
DB 301 FRQVLAVGVRHLLKRTPRPASTHSSLDVAGVHQLKRTPRPASTHNGSVDTENDSCLQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 2
GP26 HUMAN
ID GP26 HUMAN STANDARD; PRT; 337 AA.
AC Q8NUV2.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable G protein-coupled receptor GPR26.
GN GPR26.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Jones G., Boulay J.L., Maier D., Merlo A.;
RT "The 10q25.3-26.1 gene encoding the orphan G protein-coupled receptor
RT GPR26 is epigenetically silenced in human gliomas.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Boulay J.L., Labuhn M., Jones G., Maier D., Merlo A.;
RT "The 10q25.3-26.1 gene encoding the orphan G protein-coupled receptor
RT GPR26 is epigenetically silenced in human gliomas.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
CC EMBL; AJ505757; CAD44281.1; -.
CC Genew; HGNC:4481; GPR26.
CC MIM; 604847; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; FALSE_NEG.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 10
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 11 31
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 47
FT TRANSMEM 48 68
FT DOMAIN 69 81
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 82 102
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 103 123
FT TRANSMEM 124 144
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 145 188
FT TRANSMEM 169 189
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 267 276
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 297
FT DOMAIN 298 337
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 79 156
FT BY SIMILARITY.
SQ SEQUENCE 337 AA; 37603 MW; 4E04D371505F6D01 CRC64;

Query Match 45.6%; Score 848; DB 1; Length 337;
Best Local Similarity 52.0%; Pred. No. 3.8e-56;
Matches 170; Conservative 52; Mismatches 101; Indels 4; Gaps 1;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
DB 1 MNSWDAGLAGLLVGTNGVSLLSNALVLLCLHSADIRQAPALFTLITCGNLLCTVNM 60
QY 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPFLRYAGRLRP 120
DB 61 PLTLAGVVAQRQPGADRLCLAAFLDTFLAANSMLSMALSIDRWVAVVFLSYRAKWL 120
QY 121 RVAGLLGCAGQSLAFSGAALGCSWLGYSYSAFASCSLRLPPEPRPFAATLHVG 180
DB 121 RDAAIMVAVTWLHALTFPAALALSWLGFHQYASCTICSSRRPDELRFVFTGFAHLS 180
QY 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCQLQKRRHRAT 240
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Db 181 FLLSFVLCCTVLKVLKVARFCKRIDVTMTQTLVLLVDLHPSVERCLESEKRRQRAT 240
QY 241 RKIGIAIATFLICFAPYVMTLAEVLVFFVVAQNGILSKCLTYSKAVADPTYSLLRRP 300
Db 241 KXISTFIGFLVCFAPYVITRLVELFSTVPIGSHGVLSKCLAYSKAASDPFVYSLRHQ 300
QY 301 FRQVLGAVHRLKTPRPASTHDSL 327
Db 301 YRSCKEILNRLHR-----RSIHSSGL 323

RESULT 3
GP26 RAT STANDARD; PRT; 337 AA.
ID Q9QX13;
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable G protein-coupled receptor GPR26.
GN GPR26.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=20149952; PubMed=10684976;
RX Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT "Cloning and characterization of additional members of the G protein-
coupled receptor family.";
RL Biochim. Biophys. Acta 1490:311-323 (2000).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in extracts of several brain regions
including striatum, pons, cerebellum and cortex. Not detected in
numerous peripheral tissue extracts, except in testis. In the
brain, detected in cortical structures including the anterior
cingulate area, posterior cingulate and the frontoparietal,
somatosensory and piriform cortices. Prominent also in the
olfactory tubercle, the islands of Calleja, ventromedial and
posterior nuclei of the hypothalamus, the medial septal nucleus,
nucleus of the diagonal band and the ventral tegmental area.
CC Localized also to hippocampal structures, with signals strongest
over the CA2 and CA3 regions of Ammon's horn and less so over the
dentate gyrus. Expressed in the caudate putamen only in its most
caudal portion, with a decreasing gradient of signal from the
dorsal to ventral aspect. Strong expression associated with a
single pontine structure, the inferior olivary nucleus.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
CC EMBL: AF208288; AAF21012.1; -.
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC InterPro: IPR000169; SHprot_acsite.
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1.1; FALSE_NEG.
CC PROSITE; PS00262; G-PROTEIN RECEPT_F1.2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 10 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 11 31 1 (POTENTIAL).
CC DOMAIN 32 47 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 48 68 2 (POTENTIAL).

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FT DOMAIN 69 81 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 82 102 3 (POTENTIAL).
FT DOMAIN 103 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 144 4 (POTENTIAL).
FT DOMAIN 145 168 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 169 189 5 (POTENTIAL).
FT DOMAIN 190 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266 6 (POTENTIAL).
FT DOMAIN 267 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 337 CYTOPLASMIC (POTENTIAL).
FT DISULFID 79 156 BY SIMILARITY.
SQ SEQUENCE 337 AA; 37804 MW; CD7E2381F085F2DD CRC64;

Query Match 44.3%; Score 823; DB 1; Length 337;
Best Local Similarity 49.1%; Pred No. 2.7e-54;
Matches 164; Conservative 58; Mismatches 106; Indels 6; Gaps 2;

QY 1 MGPEALLAGLVVLAVALLSNALVLLCCYSAELRTRASGVLLVNLSHGLLLAALDM 60
Db 1 MNSWDAGLAGLVGTIGVLSLSNGLVLLCLLHSGADIRROAPALFTLMLTCGNLLCTVNM 60

QY 61 PFTLLGWRGRTSPAGCAQVIGFLDTFLASNAALSVAALSADOMLAVGPELAYAGRLRP 120
Db 61 PTLTAGVVAQRQFAGDRLCRLAFLDTFLAANSMLSNAALSIDRWVAVFELSYRAQRL 120

QY 121 RYAGLLGCAGQSLAFSGAALGCSMLGYSSAFASCSRLRPPERPRFAATATLHVG 180
Db 121 RDAAFVAVYTLHALTPATALALSMLGPHQLYASCTLCSSRPDERLRFVFTSAPHALS 180

QY 181 FVLPLAVLCITSLQVHVARHRCQMDVTMKALALLADLHPSVRCCLQCKRRHREAT 240
Db 181 FLSFVLCITSLYKLVKVARFCHKRIDVTMTQTLVLLVDLHPSVERCLESEKRRQRAT 240

QY 241 RKIGIAIATFLICFAPYVMTLAEVLVFFVVAQNGILSKCLTYSKAVADPTYSLLRRP 300
Db 241 KXISTFIGFLVCFAPYVITRLVELFSTVPIGSHGVLSKCLAYSKAASDPFVYSLRHQ 300

QY 301 FRQVLGAVHRLKTPRPASTHDSLDVAGMVH 334
Db 301 YRSCKEILNRLHR-----RSIH--SVGLTGDSH 328

RESULT 4
GP26 MOUSE STANDARD; PRT; 337 AA.
ID Q8BZA7; Q80T55; Q8BXZ5;
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable G protein-coupled receptor GPR26.
GN GPR26.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=CS7BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaigo I., Osato N., Saito R., Nogi A., Schonbach C., Gojobori T.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Batalov S., Beisel K.W.,
RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Cousins S.,
RA Blake J.A., Bradt D., Brusci V., Ciothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guetinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

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RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi I., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [2].

RP SEQUENCE OF 117-291 FROM N.A.
RX MEDLINE=22584407; PubMed=12679517;
RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergmann J.E., Gaitanaris G.A.;
RT "The G-protein-coupled receptor repertoires of human and mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).

CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Exclusively expressed in the brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC EMBL; AK036100; BAC29305.1; -;
DR EMBL; AK042755; BAC31354.1; -;
DR EMBL; AY255585; AA085097.1; -;
DR MGD; MGI:2441758; Gpr26.
DR InterPro; IPR000169; GPCR_Rhodopsn.
DR InterPro; IPR000169; SHPOT_acsite.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 10 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 11 31 (POTENTIAL).
FT DOMAIN 32 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 2 (POTENTIAL).
FT DOMAIN 69 81 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 82 102 3 (POTENTIAL).
FT DOMAIN 103 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 144 4 (POTENTIAL).
FT DOMAIN 145 168 5 (POTENTIAL).
FT TRANSMEM 169 189 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 190 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266 6 (POTENTIAL).
FT DOMAIN 267 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 337 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 338 356 BY SIMILARITY.
FT DISULFID 79 156 C -> R (IN REF. 2).
FT CONFLICT 156 156
SQ SEQUENCE 337 AA; 37746 MW; CD7CF15744E722DD CRC64;

Query Match 44.2%; Score 822; DB 1; Length 337;
Best Local Similarity 49.1%; Pred. No. 3.3e-54;
Matches 164; Conservative 57; Mismatches 107; Indels 6; Gaps 2;

QY 1 MCGPGLAGLVVWYVALVLSNALVLCAYSAELRTRASGVLLVNLGLHLLAALDM 60

DB 1 MNSWDAGLGLLVGTIGVYLLSNGLVLLCLLHLSADIRERQAPALFTLNTCGNLLCTVVM 60
QY 61 PFTLLGVNRGTPSPAGCAQVIGLDTFLASNAISVAALSADQWLAVGFPFLYAGRIEP 120
DB 61 PUTLAGVVAQFAGDRUCRLAAFLDTFLAANSMLSMAALSIDRWVAVVFLSYRAKMKRL 120
QY 121 RVAGLLLGCAWGCQSILAFSGAALGCSWLGYSFAFASCSLRLPPEPRPFAAFTATLHVG 180
DB 121 RDAAPWAVYTWLHALTFPATLALSWLGFHQLYASCTLCSSRRPDERLRFVFTSAFHLS 180
QY 181 FVLPLAVLCLTSLOVHRVARHCQMDVTWKALLADLHPSVQRCLIOQKRRHEAT 240
DB 181 FLSFVLVLCFTYLVKLVKVARFHCRIQVITQTLVLLVDIHPSVRERCELEQKRRQBAT 240
QY 241 RKIGIAIATFLICFAPYVYMTLAEVPPVTVAQWGLSKCLTYSKAVADFTYSLLRP 300
DB 241 KKISTFGLTFLVCFAPYVITRIVELFSTAPIGSHGVLSKCLAYSKAASDFVYSLRHQ 300
QY 301 FQVLGAMVHRLKRTPRPASTHSSLDVAGNVH 334
DB 301 YRRSCKELNRIENR---RSLH--SVGLTGDSH 328

RESULT 5
SH6_MOUSE STANDARD; PRT; 440 AA.
AC Q9RIC8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor).
GN HTR6.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Brain;
RX MEDLINE=21290977; PubMed=11408289;
RA Kohen R., Fashingbauer L.A., Heidmann D.E.A., Guthrie C.R.,
RA Hamblin M.W.;
RT "Cloning of the mouse 5-HT6 serotonin receptor and mutagenesis
RL studies of the third cytoplasmic loop.";
CC Brain Res. Mol. Brain Res. 90:110-117 (2001).
CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS
CC A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AF134158; AAD46490.1; -;
DR MGD; MGI:1196627; Htr6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).

FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 267 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 268 292 6 (POTENTIAL).
FT DOMAIN 293 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 322 7 (POTENTIAL).
FT DOMAIN 323 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CARBOHYD 3 9 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 440 AA; 46998 MW; 4440CDBE01FEF0C CRC64;

Query Match 13.2%; Score 245.5; DB 1; Length 440;
Best Local Similarity 25.1%; Pred. No. 3e-11;
Matches 100; Conservative 68; Mismatches 174; Indels 57; Gaps 15;

QY 2 GPGEA-----LLAGLLVMVLAALLSNALVLLCCAYSAELRTFASGVLLVNLGLH 53
DB 16 GPGEPPAPGSGWVAALCVVLTAAANSLTALICTOPALRNT--SNFFLVSLTSDL 73

QY 54 LLAALDMPFTLLGVMRGTPSAPGACQVIGFDTFLASNAALSVAAALSADQWLVGFPLR 113
DB 74 MVGLVWPAMPALNLYGRVWLGCLLTWAFVWCCSASILNCLISLDYVLLLSPLR 133

QY 114 YAGRL-RPYAGLLIGCANGOSIA-----FSGAALGCSWLG--YSAFASCSL--RLPPEP 164
DB 134 YKRLMTAPRALILG-AW--SLAALASFLPLLLGHWELGKARTAPGQCRLIASLP--- 187

QY 165 ERPRFAAFTATLHAGVFLPLAVLCITSLQVHRVARRHQMDIVT-----MKALA 215
DB 188 -----YVLVAGSVTFPLPSGACFTYCYRILLAAKQAVASLTGTATAGQALETLQ 240

QY 216 LLAHLHPSVR-----QRLCLOKRRHRATKIGIAIATFLICPAPYVMTRIAELVPFTV 271
DB 241 VPRTPRPGMESADSRLLTKHRSKALKASLTGILLSMFEVFWLFFVFAVIAQAQVDCIS 300

QY 272 NAOGWILSKCLTSKAVADPFYLSLRRPFRVLAGWV-----HLLKRTPRPASTH 323
DB 301 PGLFDVLT-WLVCNSTWPIYPLFMRDFKALGFVFCVCPPEHRASPASPSWTS 359

QY 324 DSSLVAGMVHQLKRTPRPASTHNGSVDTENDSCLQQT 362
DB 360 SGAR--PGLSLQVQLPLPLPPNSDSDSA--SGTSGQLQT 395

RESULT 6
SH6 HUMAN STANDARD; PRT; 440 AA.
AC P50406; Q13640;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor).
GN HTR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Striatum;
RC MEDLINE=96102917; PubMed=8522988;
RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RA Sibley D.R., Roth B., Hamblin M.W.,
RT "cloning, characterization, and chromosomal localization of a human
RT 5-HT6 serotonin receptor";
RL J. Neurochem. 66:47-56 (1996).
RN [2]

RP SEQUENCE OF 215-280 FROM N.A.
RC TISSUE=Striatum;
RX MEDLINE=95385798; PubMed=7656980;
RA Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RT "Expression of serotonin receptor mRNAs in blood vessels.";
RL FEBS Lett. 370:215-221 (1995).
CC -I- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate cyclase. It has a high affinity for tricyclic psychotropic drugs.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed in several human brain regions, most prominently in the caudate nucleus.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; L41147; AAA92622.1; -;
DR EMBL; Z49119; CAA88929.1; -;
DR PIR; JCS520; JCS520.
DR Genew; HGNC:5301; HTR6.
DR MIM; 601109; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:004989; F: histamine receptor activity; TAS.
DR GO; GO:0007187; F: G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0007268; P: synaptic transmission; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F2_1; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 290 6 (POTENTIAL).
FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 296 320 7 (POTENTIAL).
FT DOMAIN 321 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CONFLICT 247 V -> M (IN REF. 2).
SQ SEQUENCE 440 AA; 46954 MW; C888P47650C1D2EF CRC64;

Query Match 13.2%; Score 244.5; DB 1; Length 440;
Best Local Similarity 26.1%; Pred. No. 3.6e-11;
Matches 102; Conservative 64; Mismatches 164; Indels 61; Gaps 17;

QY 2 GP-----GEALLAGLLVMVLAALLSNALVLLCCAYSAELRTFASGVLLVNLGLHLL 55
DB 18 GPSPAPGSGWVAALCVVLTAAANSLTALICTOPALRNT--SNFFLVSLTSDLMV 75

QY 56 AALDMPFTLLGVMRGTPSAPGACQVIGFDTFLASNAALSVAAALSADQWLVGFPLRYA 115
DB 76 GLVWPPAMPALNLYGRVWLGCLLTWAFVWCCSASILNCLISLDYVLLLSPLRYK 135

QY 116 GLRPP-RYAGLLIGCANGOSIA-----FSGAALGCSWLGYSAPASCSLRLPPEPRFA 170
RL J. Neurochem. 66:47-56 (1996).
RN [2]

Db 136 LRMTPERLALVLG-AW--SIAALASFLPLLGHWELGHAR-----PPVPGQCRLL 183

Qy 171 A---FTATLHVGFLPLAVLCLSLQVHRVARRHCOEMDTVT-----MKALALLADL 220

Db 184 ASLPVLVASGLTFLPSGAICFTYCRILLAAKQAVQASLTITGMAQASSETLQVPRTP 243

Qy 221 HPSVR-----QRCLQOKRRRHARKIGIATATLFCFAPVWTRLAELVFFVTVAQWG 276

Db 244 RGVESADSRRLATKSHSKALKASLTGLLGMFFVTWLPFFVANIYVQAVCDICISPOLFD 303

Qy 277 ILSKCLITYSKAVADPTYSLLRRPPROVLAGWVHRL--KRTP--RPASTHDSLDVA-- 330

Db 304 VLT-WLGCYNSMTNPIIYFLWROFKRALG-----RFLPCPCPRERQASLASPSLRSHS 358

Qy 331 ----GMVHQLKRRTPRPASTNGSVDTENDS 357

Db 359 GPRGLSLQVVLPLPLPP-----DSDSDS 382

RESULT 7

SSR4 HUMAN

ID SSR4_HUMAN STANDARD; PRT; 388 AA.

AC P31391; Q9UUY1;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Somatostatin receptor type 4 (SS4R).

GN SSR4.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93290656; PubMed=8512564;

RA Xu Y., Song J., Bruno J.F., Berelowitz M.;

RT "Molecular cloning and sequencing of a human somatostatin receptor,

RT hsSTR4.";

RL Biochem. Biophys. Res. Commun. 193:648-652(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93249256; PubMed=8483934;

RA Rohrer L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,

RA Schuele R.;

RT "Cloning and characterization of a fourth human somatostatin

RT receptor.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=93384611; PubMed=8373420;

RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda Y.,

RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;

RT "Cloning, functional expression and pharmacological characterization

RT of a fourth (hsSTR4) and a fifth (hsSTR5) human somatostatin receptor

RT subtype.";

RL Biochem. Biophys. Res. Commun. 195:844-852(1993).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=93302729; PubMed=8100352;

RA Demchyshyn L.L., Srikanth C.B., Sunahara R.K., Kent G., Seeman P.,

RA van Tol H.H.M., Panatier R., Patel Y.C., Niznik H.B.;

RT "Cloning and expression of a human somatostatin-14-selective receptor

RT variant (somatostatin receptor 4) located on chromosome 20.";

RL Mol. Pharmacol. 43:894-901(1993).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Alameda J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark M., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaselathio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.I., Martin S.I., McConachie D.J., McLeay K., McMurray A.A.,

Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,

Skuce C.D., Sycamore N., Soderlund C., Steward C.A., Sulston J.E.,

Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).

CC -I- FUNCTION: Receptor for somatostatin-14. The activity of this

CC receptor is mediated by G proteins which inhibits adenylyl

CC cyclase. It is functionally coupled not only to inhibition of

CC adenylate cyclase, but also to activation of both arachidonate

CC release and mitogen-activated protein (MAP) kinase cascade.

CC Mediates antiproliferative action of somatostatin in tumor cells.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: Specifically expressed in fetal and adult

CC brain, lung tissue, stomach, and in lesser quantities in the

CC kidney, pituitary and adrenals.

CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC

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CC -----

CC EMBL: D16826; BAA04106.1; -

CC EMBL: L14856; AAA36623.1; -

CC EMBL: L07833; AAA60565.1; -

CC EMBL: L07061; -; NOT ANNOTATED CDS.

CC EMBL: AL049651; CAB51953.1; -

CC PIR: JN0605; JN0605.

CC HSP: P02699; IBOJ.

CC Genew: HGNC:11333; SSTR4.

CC MIM: 182454; -

CC GO: GO:0003887; C:integral to plasma membrane; TAS.

CC GO: GO:0004994; F:somatostatin receptor activity; TAS.

CC GO: GO:0007187; P:G-protein signaling, coupled to cyclic nucl.; TAS.

CC GO: GO:0008285; P:negative regulation of cell proliferation; TAS.

CC InterPro: IPR000276; GPCR_rhodpsn.

CC Pfam: PF00001; 7tm.1.1.

CC PRINTS: PR00237; GPCRHOPOPSN.

CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.

CC PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein;

CC Multigene family; Lipoprotein; Palmitate; Phosphorylation;

CC Polymorphism.

CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 47 73 1 (POTENTIAL).

CC DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 84 104 2 (POTENTIAL).

CC DOMAIN 105 120 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 121 142 3 (POTENTIAL).

CC DOMAIN 143 161 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 162 185 4 (POTENTIAL).

CC DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 209 232 5 (POTENTIAL).

CC DOMAIN 233 260 CYTOPLASMIC (POTENTIAL).


```

FT TRANSMEM 261 280
FT DOMAIN 281 291
FT TRANSMEM 292 314
FT TRANSMEM 315 338
FT CARBOHYD 24 24
FT DISULFID 119 198
FT LIPID 327 327
FT VARIANT 83 83
FT CONFLICT 284 284
FT CONFLICT 321 321
FT CONFLICT 365 365
FT SEQUENCE 388 AA; 41894 MW; 8BCDD69B5F3BC2F5 CRC64;

Query Match 13.1%; Score 243.5; DB 1; Length 388;
Best Local Similarity 25.5%; Pred. No. 3.8e-11;
Matches 84; Conservative 55; Mismatches 124; Indels 67; Gaps 10;

QY 2 GPGEALLAGLL-----VNVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISGLHLL 55
D5 38 GFGDARAAGMVAIOCTYALVCLVGLVGNALVIFVILRYAKMT-ATNYYLLNLAVADELF 96
QY 56 AALDMPFTLLGVMGRGTSAPGACQVIGFLDTFLASNAALSVAALSADQWLAQVFLRYA 115
D5 97 -MLSPFFVASSAALRHWPFSGVLCRAVLSDVGLNMFVSFCLTVLSVDYVAVVHPGAA 155
QY 116 GLRLPRYAGLLGCAGGOSL-----AFSGAALGCS--WLGYSASFASCSLR 159
D5 156 TYRERSVAKLNLGVNLASLLVTLPIAFADTRPARGGQAVACNLQW----- 202
QY 160 LPPEPERPFAAFTLHAGVGLVPLAVCLTSQVHRVARHRCQMDTVTKALALLAD 219
D5 203 ----PFPAMSAVFFVYVTFLLGFLLEPLAIGL-----CYLLIVGKRAVALRAG 246
QY 220 LHPVSQRCLIOKRRRRHRRATKIGIATATFLICFAPVMTRELAEVFPVTVNAQWGLS 279
D5 247 WQ-----QRRSEKIKITLVLMVVVFLVCLWMPFVVVQLNLV-VTSLDATVHVS 296
QY 280 KCLTVSKAVADPFTVSL-----RRPFRQVL 305
D5 297 LILSVANSACNDILYGLFLSDNFRSFRVFL 326

RESULT 8
SH6_RAT STANDARD; PRT; 436 AA.
AC P31388;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor)
GN (ST-B17).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Striatum;
RX MEDLINE=93196508; PubMed=7680751;
RA Monsma F.J. Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;
RT "Cloning and expression of a novel serotonin receptor with high
RT affinity for tricyclic psychotropic drugs."
RL Mol. Pharmacol. 43:320-327(1993).
RN [2];
RN SEQUENCE FROM N.A.
RX MEDLINE=93277562; PubMed=8389146;
RA Ruat M., Traiffort E., Arrang J.-M., Tardivel-Lacombe J., Diaz J.,
RA Leurs R., Schwartz J.-C.;
RT "A novel rat serotonin (5-HT6) receptor: molecular cloning,
RT localization and stimulation of cAMP accumulation."
RL Biochem. Biophys. Res. Commun. 193:268-276(1993).

```

```

[3] SEQUENCE FROM N.A.
RP STRAIN=Wistar;
RA Martini R.;
RL Submitted (XX-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This is one of the several different receptors for 5-
CC hydroxytryptamine (serotonin), a biogenic hormone that functions
CC as a neurotransmitter, a hormone, and a mitogen. The activity of
CC this receptor is mediated by G proteins that stimulates adenylyate
CC cyclase. It has a high affinity for tricyclic psychotropic drugs.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Localized exclusively in the central nervous
CC system, predominantly in the corpus striatum but also in various
CC limbic and cortical regions.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L03202; AAA40618.1; -
CC EMBL; S62043; AAB26908.1; -
CC EMBL; L19656; AAA40611.1; -
CC PIR; I57942; I57942.
CC JN0591; JN0591.
CC InterPro; IPR000276; GPCR_Rhodopn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 57 1 (POTENTIAL).
CC DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 65 85 2 (POTENTIAL).
CC DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 101 122 3 (POTENTIAL).
CC DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 145 166 4 (POTENTIAL).
CC DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 185 208 5 (POTENTIAL).
CC DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 266 295 6 (POTENTIAL).
CC DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 296 320 7 (POTENTIAL).
CC DOMAIN 321 436 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 9 9 N-LINKED (GLCNAC... ) (POTENTIAL).
CC DISULFID 99 180 BY SIMILARITY.
CC CONFLICT 57 57 L -> V (IN REF. 1).
CC CONFLICT 336 436 PCVHCPEHRPALPPPCGFLTAVPDQASACRCLCLCRQ
TOIOTLOQAPRACSSQSPFCCLERPGTTPRPPGGLPWT
SLSOTLWLSRYGRHSVPP -> HASTVPRSTGQCLPLHV
DLISQRCQTRPQQVLLALPLPNSDSASGSGSLQLTRQ
LLLPGEATDRPPFTRATTVNFFVFTDSVEPEIRPPLSP
VN (IN REF. 1).
SQ SEQUENCE 436 AA; 46922 MW; 6BC00F6A3CBASFB4 CRC64;

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Query Match 12.9%; Score 239; DB 1; Length 436;
Best Local Similarity 25.7%; Pred. No. 9.2e-11;
Matches 85; Conservative 58; Mismatches 146; Indels 42; Gaps 11;

QY 2 GPGEA-----LLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISGLH 53
D5 16 GPGFPAPGSGGWAAALCVIVLTAANSLVILICTQPALRNT--SNFFLVSLFTSDL 73
QY 54 LLAALDMPFTLLGVMGRGTSAPGACQVIGFLDTFLASNAALSVAALSADQWLAQVFLR 113
D5 74 MVGLVVMPPAMLNALYGRVWLARGLCLLMTAFDVMCCSAILNCLISLDRLVLLSPUR 133

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QY 114 YAGRL-RPYAGLLIGCAWGSLA-----FSGAALGCSWLGVSFAFASCSRLRLPEPERPR 168
 DB 134 YKRWAPRALALIG-AW-SLAALASFLPLLLGHWELGKART-----PARGOQR 181
 QY 169 FAA---FTATLHVGFLVPLAVCLTSLQVHRVARHCQMDVT-----WKALALLA 218
 DB 182 LLASLPFLVAGVTFPLPSGAICFTYCRILLARKQAVQVASLTGTAGQALLETLOVPR 241
 QY 219 DLHESVR---ORCLIQKRHRHATRKIGIAITATFICFAPYVMTSLAELVFPVTNAQ 274
 DB 242 TPRMESADSRRLATHKSRALKASUTGLGILGFMFFVWLPFPFVANIAQVCDICSPGL 301
 QY 275 WGIILSKLTYSKAVADPFTYSLRRPFRQVL 305
 DB 302 FDLVT-WLGYCNSTWNPPIIYPLFMRDFKRAL 331
 RESULT 9
 HH2R_CAVPO STANDARD; PRT; 359 AA.
 AC P47747;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Histamine H2 receptor (H2R) (Gastric receptor I).
 GN HR42.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley; TISSUE=Liver;
 RA Traifort E.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The H2 subclass of histamine receptors mediates gastric
 CC acid secretion. The activity of this receptor is mediated by G
 CC proteins which activate adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U25440; AAA65713.1; -.
 DR PIR; JC4120; JC4120.
 DR HSP; P29274; 1MWH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 KW Palmitate.
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 23 44 1 (POTENTIAL).
 FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 81 2 (POTENTIAL).
 FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 93 114 3 (POTENTIAL).
 FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 135 159 4 (POTENTIAL).
 FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 181 204 5 (POTENTIAL).
 FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 258 6 (POTENTIAL).
 FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 268 289 7 (POTENTIAL).
 FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).
 FT SITE 98 ESSENTIAL FOR HISTAMINE BINDING (BY
 FT SIMILARITY).
 FT SITE 186 ESSENTIAL FOR TIOIDINE BINDING AND
 FT IMPLICATED IN HISTAMINE BINDING (BY
 FT SIMILARITY).
 FT SITE 190 IMPLICATED IN HISTAMINE BINDING (BY
 FT SIMILARITY).
 FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 91 174 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40556 MW; 58DB81BD8FC3C0E9 CRC64;
 Query Match 12.5%; Score 232.5; DB 1; Length 359;
 Best Local Similarity 22.0%; Pred. NO. 2.3e-10;
 Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;
 QY 11 LLVMTLAVALLSNALVLLCCAVSABLRTASGVLLVNLISLGHLLIAALDMEFTLLGVNRG 70
 DB 24 ILIILITVAGVVVCLAVGLNRLRS-LTNCFVSLAVTDLLGLLVLPFSAIYQLSC 82
 QY 71 RTPSAPGACQVIGFLDTFLASNAALSVLAASADQWLVGFFLYAGRLRPRYAGLLLOCA 130
 DB 83 KWSFKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVTDELRYEVLITPARVAISLVFI 142
 QY 131 WQSIAFSGAALGCSWLGV-----SSAFASCSLRLPEPERPFAATLHVGFLVLP 184
 DB 143 WISITLFLSLHGLNSRNETSKNDIVKCKGVN-----EVYGLVDGLVTFYLP 194
 QY 185 LAVLCUTSLQVHRVARHCQMDTV-TMKALLADLHPSVQRCLIOCKRRRHATRKI 243
 DB 195 LLIMCITYFRIFKIAREQARRINHIGSWKAATI-----REHKATVTL 236
 QY 244 GIAIATFELICFAPYVMTSLAELVFPV-----TVNAQWGLSKLTYSKAVADPFTYS 295
 DB 237 AAVMGAFILCWFPY-----FTVFYRGLKGDADVNEFEDVWLVGLYANSALPIYA 289
 QY 296 LLRRPFRQVLAVGWVHRLKRTPRPASTHDSLSL 327
 DB 290 ALNRDPTA---YHQLFCCRLASHSHSETSL 317
 RESULT 10
 SH4_MOUSE STANDARD; PRT; 388 AA.
 AC P97288; O89003; O89004; Q9R2A4;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 5-hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
 GN HTR4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss; TISSUE=Brain;
 RX MEDLINE=97102706; PubMed=8946946;
 RA Claeysen S., Sebben M., Journot L., Bockaert J., Dumuis A.;
 RT "cloning, expression and pharmacology of the mouse 5-HT(4L)
 RL FEBS Lett. 398:19-25 (1996).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RA Dumuis A.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E)).
 RC STRAIN=Swiss; TISSUE=Brain;
 RX MEDLINE=99127199; PubMed=9928238;
 RA Claeysen S., Paye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;

RT "5-HT4 receptors: cloning and expression of new splice variants."; Ann. N.Y. Acad. Sci. 861:49-56(1998).
 RL [4]
 RN
 RP SEQUENCE FROM N.A. (ISOPFORM 5-HT4(F)).
 RC TISSUE=Brain;
 RX MEDLINE=99238795; PubMed=10220570;
 RA Claeysen S., Sebben M., Becamel C., Bockaert J., Dumuis A.;
 RT "Novel brain-specific 5-HT4 receptor splice variants show marked
 RT constitutive activity: role of the C-terminal intracellular domain."; Mol. Pharmacol. 55:910-920(1999).
 RL
 CC -!- FUNCTION: This is one of the several different receptors for 5-
 CC hydroxytryptamine (serotonin), a biogenic hormone that functions
 CC as a neurotransmitter, a hormone, and a mitogen. The activity of
 CC this receptor is mediated by G proteins that stimulates adenylyate
 CC cyclase (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=P97288-1; Sequences=Displayed;
 CC Name=5-HT4(A);
 CC IsoId=P97288-2; Sequence=VSP_001851;
 CC Name=5-HT4(E);
 CC IsoId=P97288-3; Sequence=VSP_001852;
 CC Name=5-HT4(F);
 CC IsoId=P97288-4; Sequence=VSP_001853;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; Y09585; CAA70773.1; -;
 CC EMBL; Y09587; CAA70775.1; -;
 CC EMBL; Y09588; CAA70776.1; -;
 CC EMBL; A0011369; CAA03598.1; -;
 CC HSSP; P29274; 1MMH.
 CC MGD; MGI:109246; Htr4.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHOODPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
 FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 20 40 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 58
 FT TRANSMEM 59 79
 FT DOMAIN 80 93 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 94 116
 FT DOMAIN 117 137 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 138 158
 FT DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 193 213
 FT DOMAIN 214 260
 FT TRANSMEM 261 281
 FT DOMAIN 282 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 315
 FT DOMAIN 316 388 CYTOPLASMIC (POTENTIAL).
 FT BY SIMILARITY.
 FT S-palmitoyl cysteine (By similarity).
 FT LIPID 329
 FT DISULFID 329
 FT CARBOHYD 93 184
 FT LIPID 329
 FT VARSPLIC 360
 FT DAVECGGQWESRCHLTATSPLVAAQPSDT -> YIVLHSGH
 FT HOEKLPIHNDPESLESCF (in isoform
 FT 5-HT4(A)).
 FT /FTId=VSP_001851.
 FT DAVECGGQWESRCHLTATSPLVAAQPSDT -> SFPLLR
 FT NRPV (in isoform 5-HT4(E)).
 FT
 FT VARSPLIC 359 388
 FT DAVECGGQWESRCHLTATSPLVAAQPSDT -> SFPLLR
 FT NRPV (in isoform 5-HT4(E)).
 FT

FT VARSPLIC 360 388 /FTId=VSP_001852.
 FT DAVECGGQWESRCHLTATSPLVAAQPSDT -> PVPV (in
 FT isoform 5-HT4(F)).
 FT /FTId=VSP_001853.
 SQ SEQUENCE 388 AA; 43931 MW; F84163F39BA115B0 CRC64;
 Query Match 12.5%; Score 232; DB 1; Length 388;
 Best Local Similarity 22.1%; Pred. NO. 2.7e-10;
 Matches 83; Conservative 72; Mismatches 166; Indels 54; Gaps 10;
 QY 5 EALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDMPFTL 64
 Db 19 KVVLLTFLAVILMAILGNLLVWVAVCRDRQLRKIKTYFIVSLAPADLLVSLVMPFGA 78
 QY 65 LGVMGRTPSAPGACQVIGFLDTPLASNAALSVAALSADQWLAVGF-PLRYAGRLPRYA 123
 Db 79 IELVQDIWAYGEMFCLVTRTSLDVLTTASIFHLCCISLDRYAICQPLVYRNKMTPLRI 138
 QY 124 GLILGCAGQSLAFSGAALGCSW-----LGYSSAFASCSLRLLPPEPPEPFA 170
 Db 139 ALMLGGCVLPWFISFLPIMGQNNNIGIVDVIEKRFESHNSNSTWCVFVW---NKP--- 191
 QY 171 APTATLHAGVFLPLAVLCITSLQVHRVARRHCQMDTV-----TWKALLALLDHPSVR 225
 Db 192 -YAITCSVVAFYIPFLLMVLAIVYVYTAKEHAQQIQMLQKAGATSESRPQADQSHTR 250
 QY 226 QRCILQOKRRHEATRKIGIATLITELICFAPYVMTRLAELVPEV--TVNAQWGLSKCLT 283
 Db 251 M-----RTETKAKTLCVIMGCFECFCWAPFVTVIVD--PFIDYVPEQWTAIWLGG 301
 QY 284 YSKAVADPFTYSLLRPFQVLAGMVRLLKRTPRPASTHDSLSLDVAGVMVHQLKKT-PR 342
 Db 302 YINSGLNPFYAFYLFNKSFRRAFLILCCDDERYKRP-----PILGQTVPC 346
 QY 343 PASTHNGSVDTENDS 357
 Db 347 STTTINGSTHVLKDA 361
 RESULT 11
 SSRS_HUMAN
 ID SSRS_HUMAN STANDARD; PRT; 364 AA.
 AC P35346; P34988; Q9UUI5;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Somatostatin receptor type 5 (SS5R).
 GN SS5R5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195267; PubMed=7908405;
 RA Panetta R., Greenwood M.T., Warszynska A., Demchysyn L.L., Day R.,
 RA Niznik H.B., Srikant C.B., Patel Y.C.;
 RT "Molecular cloning, functional characterization, and chromosomal
 RT localization of a human somatostatin receptor (somatostatin receptor
 RT type 5) with preferential affinity for somatostatin-28";
 RL Mol. Pharmacol. 45:417-427(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93384611; PubMed=8373420;
 RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Someya Y.,
 RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;
 RT "Cloning, functional expression and pharmacological characterization
 RT of a fourth (hSS4R) and a fifth (hSS5R5) human somatostatin receptor
 RT subtype."; Biochem. Biophys. Res. Commun. 195:844-852(1993).
 RL Biochem. Biophys. Res. Commun. 195:844-852(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359492; PubMed=8078491;

RA O'Carroll A.-M., Raynor K., Lolait S.J., Reisine T.;
 RT "Characterization of cloned human somatostatin receptor SSTR5.";
 RM Mol. Pharmacol. 46:291-298(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Paden J.F., Lloyd C., Horeley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT MB of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Baguley C.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for somatostatin 28 and to a lesser extent for
 CC somatostatin-14. The activity of this receptor is mediated by G
 CC proteins which inhibit adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Adult pituitary gland, heart, small intestine,
 CC adrenal gland, cerebellum and fetal hypothalamus. No expression
 CC in fetal or adult kidney, liver, pancreas, uterus, spleen, lung,
 CC thyroid or ovary.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; L14865; AAA20828.1; -;
 CC EMBL; D16827; BAA04107.1; -;
 CC EMBL; AE006466; AAK61286.1; -;
 CC EMBL; AL031713; CAB56181.1; -;
 CC PIR; I57955; I57955.
 CC PIR; JN0763; JN0763.
 CC HSSP; F02699; I988.
 CC Genew; HGNC:11334; SSTR5.
 CC MIM; 182455;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004994; P: somatostatin receptor activity; TAS.
 CC GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. . . ; TAS.
 CC GO; GO:0008285; P: negative regulation of cell proliferation; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsin
 CC PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate; Phosphorylation.
 CC DOMAIN 1 38
 CC TRANSFAM 39 66
 CC TRANSFAM 67 76
 CC TRANSFAM 77 101
 CC TRANSFAM 102 113
 CC TRANSFAM 114 135
 CC TRANSFAM 136 157
 CC TRANSFAM 158 178
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FEBS Lett. 324:127-130(1993).
[4]
SEQUENCE OF 392-408 FROM N.A.
Granneman J.G., Lahmans K.N., Rao D.D.;
"Advent and human beta 3-adrenergic receptor genes contain an intron
within the protein-coding block.";
Mol. Pharmacol. 42:964-970(1992).
[5]
VARIANT ARG-64.
MEDLINE-95334045; PubMed=7609732;
Clement K., Vaisse C., Manning B.S.J., Basdevant A., Guy-Grand B.,
Ruiz J., Silver K.D., Shuldiner A.R., Froquel P., Strosberg A.D.;
"Genetic variation in the beta 3-adrenergic receptor and an increased
capacity to gain weight in patients with morbid obesity.";
New Engl. J. Med. 333:352-354(1995).
[6]
VARIANT ARG-64.
MEDLINE-96361936; PubMed=8721782;
Fujiwara T., Ikegami H., Yanato E., Takekawa K., Nakagawa Y.,
Hamada Y., Oga T., Ueda H., Shintani M., Fukuda M., Ogiwara T.;
"Association of Trp64Arg mutation of the beta3-adrenergic-receptor
with NIDDM and body weight gain.";
Diabetologia 39:349-352(1996).
[7]
VARIANT ARG-64.
MEDLINE-96217306; PubMed=8641219;
Candelore M.R., Deng L., Tota L.M., Kelly L.J., Cascieri M.A.,
Strader C.D.;
"Pharmacological characterization of a recently described human beta
3-adrenergic receptor mutant.";
Endocrinology 137:2638-2641(1996).
[8]
VARIANTS ARG-64 AND MET-265
MEDLINE-99318094; PubMed=10391210;
Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
Cooper R., Lipshutz R., Chakravarti A.;
"Patterns of single-nucleotide polymorphisms in candidate genes for
blood-pressure homeostasis.";
Nat. Genet. 22:239-247(1999).
CC -!- FUNCTION: Beta-adrenergic receptors mediate the catecholamine-
induced activation of adenylate cyclase through the action of G
proteins. Beta-3 is involved in the regulation of lipolysis and
thermogenesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed mainly in adipose tissues.
CC -!- POLYMORPHISM: The variant Arg-64 seems to be associated with
weight gain (obesity) and to be also associated with
susceptibility to non-insulin-dependent diabetes mellitus (NIDDM).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; M29932; AAA35550.1; ALT_TERM.
EMBL; X72861; CAA51383.1; -.
EMBL; X70811; CAA50141.1; -.
EMBL; X70812; CAA50142.1; ALT_SEQ.
EMBL; X70812; CAA50143.1; ALT_SEQ.
EMBL; S53291; AAB24837.1; -.
PIR; I57941; I57941.
PIR; S33751; ORHUB.
HSP; P29274; 1MH.
Genew; HGNC:288; ADRE3.
MIM; 109691; -.
GO; GO:0008887; C:integral to plasma membrane; TAS.
GO; GO:0015052; F:beta3-adrenergic receptor activity; TAS.
GO; GO:0005975; P:carbohydrate metabolism; TAS.

DR GO; GO:0006091; P:energy pathways; TAS.
DR GO; GO:0006112; P:energy reserve metabolism; TAS.
DR GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate;
Polymorphism; Diabetes mellitus; Obesity.
KW DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 37 63 1 (POTENTIAL).
FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT DOMAIN 92 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 178 4 (POTENTIAL).
FT DOMAIN 179 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 225 5 (POTENTIAL).
FT DOMAIN 226 292 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 293 314 6 (POTENTIAL).
FT DOMAIN 315 326 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 327 347 7 (POTENTIAL).
FT DOMAIN 348 408 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 189 BY SIMILARITY.
FT LIPID 361 361 S-palmitoyl cysteine (By similarity).
FT VARIANT 64 64 W -> R (in dbSNP:4994).
FT VARIANT 265 265 T -> M (in dbSNP:4995).
FT VARIANT 265 265 /FTid=VAR_003456.
FT SEQUENCE 408 AA; 43519 MW; E98BD6C130DD977B CRC64;
Query Match 12.4%; Score 230.5; DB 1; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.7e-10;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVMVLAVALLS---NALVLCCAYSAELRTRAGVLLVNLGLHLLAAL 58
DB 34 PWEALAGAL---LALAVLATVCGNLLVIVAIWTPRLQT-MTNVFTSLAAADLVWGLL 89
QY 59 DMPFTLLGVNMRTPSAPGACQVIGFLDTFLASNAALSVAALSADOWLAVGFLPLRYAGRL 118
DB 90 WPPAATLALTHWPLGATGCELWTSVDVLCVTASITLTCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRYAGLLLCANGQSALFSGALGCSW--LGYSASFASCSLRLPPEPEPRFAATL 176
DB 150 TKRCARTAVVLMVWSAAVSFAFIMSQMRVGDADAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFLPLAVLCITSLQVHRVARRHC-----QRMDTVTMKALA--- 215
DB 203 PYVLSSVSFYLPLLVMLFVYARFVATRLRLGELGRFPPEESPAPSRSLAPAP 262
QY 216 ----LADLHPSVRQCLIOQKRRHRATKIGIATATLFCAPYVMTRL-----AEL 265
DB 263 VGTCAPEGVFACGRPARLLPLREHRLCTGLINGTFLCWLFPFLANVRLAGPSL 322
QY 266 VP---FVTVAQNGILSKCLITYSKAVADPTYSL---LRPPFQVLGVMVHRLKKTTPR 319
DB 323 VFGPAFLALN--W-----LGYSANFNLICYCSDFRSFAFELLCRCGRRL---PPEP 371
QY 320 ASTHDSGLDVAGM 332
DB 372 CAAARFALPSPGV 384
RESULT 13
B3AR MACMU STANDARD; PRT; 418 AA.
ID B3AR MACMU
AC Q28524;

Matches	95;	Conservative	56;	Mismatches	149;	Indels	67;	Gaps	15
Qy	3	PGEALLAGLVWVAVALLS----	NALVLLCCAYSAELRTRASGVLLVNLISLGHLLAAL	58					
Db	34	PWAAALAGAL----	LALAVLATVGGNLLVVAITRPLQT-MTNVFTVLSAAADLVWGLL	89					
Qy	59	DMPFTLLGVNMGRTSPAGCAQVIGFELDTFLASNAALSVAALSADQWLAVGFPLRYAGRL	118						
Db	90	VVPPAATLVLTGHWPLGATGCELTWSDVLCVTASIEIETLCALADVRYLATVNTPLRYGALV	149						
Qy	119	RPRVAGLLCCAGQSLAFSGALGCSW--	LCYSSAFASCSILRLPPEPRPFAAFTATL	176					
Db	150	TKRRAAAVVLVWVVAASVPFIMSQWVRVGDAAQRCH-----	SNRCCAFASNM	202					
Qy	177	-----HVGFLVPLAVLCITLSQVHRVARRHCQMD-----	TVTMKALALLADLHPVS	224					
Db	203	PYVLLSSSVSYFLPLLVMFLVYARVFWVATRLRLRWELGRFPPESSPALSRLAPAP	262						
Qy	225	RQRCILQ-----	KERRHRATKIGIAIATFLICFAPVNTL-----	265					
Db	263	AGTCAPPEGVPCRRPARLLPLREHRLACTGLTNGTFTLCWLPFFLVNLRVLRGPGSL	322						
Qy	266	VP-----FVTVNAONGILSKCLITYSKAVADPFTYSL---	LRRPRQVLAVGVRHLKRP--	317					
Db	323	VPDEAFLALN--W-----	LGVANSAPNPLIYCRSPDFRSAPRLLCHCGGR-LPRFPCA	373					
Qy	318	--REAST 322							
Db	374	ADRFASS 380							

RESULT 14

ID	OX1R HUMAN	STANDARD;	PRT;	425 AA.
AC	O43613.			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).			
GN	HCRT1R1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98150861; PubMed=9491897;			
RA	Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,			
RA	Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,			
RA	Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,			
RA	McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,			
RA	Yanagisawa M.;			
RT	Orexins and orexin receptors: a family of hypothalamic neuropeptides			
RT	and G protein-coupled receptors that regulate feeding behavior.;			
RL	Cell 92:573-585(1998).			
RP	[2]			
RP	REVIEW.			
RX	MEDLINE=21237974; PubMed=11340621;			
RA	Hung M., Mignot E.;			
RT	"Hypocretin/orexin, sleep and narcolepsy.";			
RL	Bioessays 23:397-408(2001).			
RP	[3]			
RP	REVIEW.			
RX	MEDLINE=21178476; PubMed=11283317;			
RA	Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;			
RT	"To eat or to sleep? Orexin in the regulation of feeding and			
RT	wakefulness.";			
RL	Annu. Rev. Neurosci. 24:429-458(2001).			
CC	-I- FUNCTION: Moderately selective excitatory receptor for orexin-A			
CC	and, with a lower affinity, for orexin-B neuropeptide. Seems to be			
CC	exclusively coupled to the G(q) subclass of heteromeric G			
CC	proteins, which activates the phospholipase C mediated signaling			
CC	cascade (By similarity).			

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC EMBL; AF041243; AAC39601.1; -.
 CC Genew; HGNC:4848; HCRTR1.
 CC MIM; 602392; -.
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 CC GO; GO:0007631; P: feeding behavior; TAS.
 CC GO; GO:0007218; P: neuropeptide signaling pathway; TAS.
 CC GO; GO:0007268; P: synaptic transmission; TAS.
 CC DR InterPro; IPR000276; GPCR_Rhodopsn.
 CC DR InterPro; IPR004059; Orexin_receptor1.
 CC DR Pfam; PF00001; 7tm_1; 1.
 CC DR PRINTS; PR00237; GPCRHHODOPSN.
 CC DR PRINTS; PR01521; OREXINR.
 CC DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane.
 CC DOMAIN 1 46
 CC TRANSMEM 47 67
 CC DOMAIN 68 80
 CC TRANSMEM 81 102
 CC DOMAIN 103 119
 CC TRANSMEM 120 142
 CC DOMAIN 143 164
 CC TRANSMEM 165 185
 CC DOMAIN 186 216
 CC TRANSMEM 217 239
 CC DOMAIN 240 298
 CC TRANSMEM 299 321
 CC DOMAIN 322 336
 CC TRANSMEM 337 360
 CC DOMAIN 361 425
 CC TRANSMEM 194 194
 CC CARBOHYD 425 AA; 47521 MW; 1634083DE10CA092 CRC64;
 CC SEQUENCE 425 AA; 12.4%; Score 229.5; DB 1; Length 425;
 CC Query Match
 CC Best Local Similarity 25.3%; Pred. No. 4.5e-10;
 CC Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;
 CC -----
 CC 5 EALLAGLVNVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPFTL 64
 CC 46 EWLLIARYAVFVVALVGNLTLCVAVRNHMT-VTNYFVNLADVLVTAICLPASL 104
 CC 65 LGVNRGTPAPACQVIGFDLTFASNAALSVAAISADQWLAGVPLRYAGRLRPYAG 124
 CC 105 LVDITESWLFQHALCKVPIYQVSVSVAVLTLSFIALDRWYAIChPELLFKSTAR-RARG 163
 CC 125 LLLGCWAGQSLAFSGAALGSLGYSAPASCSLRLPPRPFRFAA-----FTA 174
 CC 164 SIIG-IWAVSLAI-----WVQAAYMECSVLPELANRTRLSVCDERWADLYPK 213
 CC 175 TLHAGVPLP-LAVLCITSQVHRVARRHCQRMDVTVMKALA-----LIADL----- 220
 CC 214 IYHSCFFIVTFLAPGLIMAYQIFRKLWGRQIPGTTGALVRNWRKPSDGLDLEQGLS 273
 CC 221 -HPSVORCL---IQKRREHRAIKIGIAIAIFLICEAP-----YVWTRLA--- 263
 CC 274 GEPQPGRAFLAEVQKARKAKMLMVLLVFLALCYLPISVNLVLRVFGMFRQASR 333
 CC 264 ELVPFVTVAQWGLSKCLTYSKAVADPFTYSLLRPFQVL-----AGMVRLL 313
 CC 334 EAVYACFTPSHW-----LVYNSAANPIYNFLSKGFREQKFAFSCCLPGLGPCGSLK 387

QY 314 KRTPRPASTHDS 325
 Db 388 APSRFSASHKS 399

 CC RESULT 15
 CC SRS5_MOUSE
 CC ID SRS5_MOUSE STANDARD; PRT; 362 AA.
 CC AC O08858; O08998;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Somatostatin receptor type 5 (SSSR).
 CC GN SRS5 OR SMSTR5.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC RC STRAIN=129/SVJ; TISSUE=Liver;
 CC RX MEDLINE=97444289; PubMed=9300821;
 CC RA Lublin A.L., Diehl N.L., Hochgeschwender U.;
 CC RT "Isolation and characterization of the gene encoding the type 5 mouse
 CC RL (Mus musculus) somatostatin receptor (msst5).";
 CC RL Gene 195:63-66(1997).
 CC RN [2]
 CC SEQUENCE FROM N.A.
 CC RP STRAIN=129/SVJ;
 CC RC Moldovan S., Demayo F., Brunicaudi F.C.;
 CC RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC RN [3]
 CC SEQUENCE FROM N.A.
 CC RP STRAIN=BALB/c; TISSUE=Liver;
 CC RA Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James R.A.;
 CC RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC RN [4]
 CC SEQUENCE FROM N.A.
 CC RC STRAIN=129/SVJ;
 CC RA Baumeister H., Roosterman D., Schafer J., Kreuzer O., Meyerhof W.;
 CC RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for somatostatin-28. The activity of this
 CC receptor is mediated by G proteins which inhibit adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; U02697; AAC53553.1; -.
 CC EMBL; AF004740; AAB61418.1; -.
 CC EMBL; AF030441; AAB86492.1; -.
 CC EMBL; AF035777; AAB88302.1; ALT_INIT.
 CC HSP; P02699; 1P88.
 CC MGD; MGI:894282; Sstr5.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate.
 CC DOMAIN 1 35
 CC TRANSMEM 36 63
 CC DOMAIN 64 73
 CC TRANSMEM 74 99
 CC DOMAIN 100 110
 CC TRANSMEM 111 132
 CC DOMAIN 133 132

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FT DOMAIN 133 154
FT TRANSMEM 155 175
FT DOMAIN 176 195
FT TRANSMEM 196 220
FT DOMAIN 221 246
FT TRANSMEM 247 272
FT DOMAIN 273 282
FT TRANSMEM 283 307
FT DOMAIN 308 362
FT CARBOHYD 13 13
FT CARBOHYD 23 23
FT CARBOHYD 185 185
FT DISULFID 109 184
FT CONFLICT 99 99
FT CONFLICT 303 305
SQ SEQUENCE 362 AA; 39948 MW; AA091DD570DFAB CRC64;

Query Match 12.3%; Score 229; DB 1; Length 362;
Best Local Similarity 25.7%; Pred. No. 4.2e-10;
Matches 95; Conservative 53; Mismatches 162; Indels 60; Gaps 13;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
Db 33 MGARAVLPVLYLLVCTVGLGGNTLVIYVLRVAKMT-VTNVYILNAVADVLF-MGL 90

QY 61 PPTLGVNRGRTPSAPGACQVIGFDFTFLASNAALSVAAALSDQWLAAGFFLRVAGRIRP 120
Db 91 PFLATQNAVSYWFFGSLCRLVMTLDGINQFTSIFCLMVMSVDRLAVVHPLRSARWRP 150

QY 121 RVAGLLGCAGQSLAFSGAALGCSWLGYSASFASCSLRLPPEPRPFPAFTATLHVG 180
Db 151 RVAKLASAAVWVFSLLMSPLL--VPADVQEGWGTCNLSW-PEPVGLWGAFTYTSVLG 207

QY 181 FVLPLAVLCLTSLQVHRVARHRCQMDVTWKALALADLHPSVRQRCLOQKRRHRAT 240
Db 208 FPGPLLIVICL-----CYLLIVVKVKAAGRVG---SSRR-----ESERKVT 246

QY 241 RKIGIAIATFLICFAPYVWTRAEI--VPFVYVNAQWGLSKCLTYSKAVADPPTYSL 297
Db 247 RMVVVVVLVFGVCLPFFIVINVLAFILPEEPTSAGLYFFVWVLSYANSCANLLYGFL 306

QY 298 ----RRPFQVLAGMVHRLK-----TPRPASTHDSLDVAGMVHQLKRTFRP 343
Db 307 SNFRQSFRKALC-----LRGYGVEDADAEPRP-----DKSGRPQTTL---PTR 349

QY 344 ASTHNGSVDT 353
Db 350 SCEANGLMQT 359
```

Search completed: May 18, 2004, 12:07:09
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:03:02 ; Search time 46 Seconds
(without alignments)
2489.850 Million cell updates/sec

Title: US-10-049-569-2

Perfect score: 1858

Sequence: 1 MGPGELLAGLLVLMVAL.....ASTHNGSVDTENDSCLOQTH 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250.5	13.5	438	11 Q63004	Q63004 rattus norv
2	246.5	13.3	390	13 Q8QG04	Q8QG04 carassius a
3	238.5	12.8	380	13 Q8DQ06	Q8DQ06 carassius a
4	237	12.8	370	13 Q8UMT5	Q8UMT5 fugu rubrip
5	237	12.8	399	5 Q8GME4	Q8GME4 caenorhabdi
6	237	12.8	402	11 Q8GME5	Q8GME5 caenorhabdi
7	233	12.5	478	11 Q8BLD9	Q8BLD9 mus musculu
8	231.5	12.5	353	13 Q9HYH3	Q9HYH3 lampetra fl
9	230.5	12.4	425	4 Q9HBV6	Q9HBV6 homo sapien
10	230	12.4	367	6 Q8MI04	Q8MI04 ovis aries
11	229.5	12.4	340	13 Q9HYH2	Q9HYH2 lampetra fl
12	229	12.3	385	11 Q9TK40	Q9TK40 mus musculu
13	228.5	12.3	437	13 Q42316	Q42316 cyprinus ca
14	227.5	12.2	367	13 Q9PVG0	Q9PVG0 carassius a
15	227.5	12.2	391	5 Q96716	Q96716 branchiost
16	227.5	12.2	477	4 Q8NEQ8	Q8NEQ8 homo sapien

17	227	12.2	380	13 Q42317	Q42317 cyprinus ca
18	226.5	12.2	358	11 Q9QX37	Q9QX37 mus musculu
19	226.5	12.2	397	11 Q9D282	Q9D282 mus musculu
20	226	12.2	390	13 Q8AXM7	Q8AXM7 carassius a
21	224	12.1	367	13 Q9PVF9	Q9PVF9 carassius a
22	223.5	12.0	371	11 Q8BK80	Q8BK80 mus musculu
23	223	12.0	387	4 Q96K10	Q96K10 homo sapien
24	222.5	12.0	385	11 Q8BQ97	Q8BQ97 mus musculu
25	222.5	12.0	447	6 Q8SPH2	Q8SPH2 sus scrofa
26	222	11.9	388	4 Q81XH9	Q81XH9 homo sapien
27	221.5	11.9	446	13 Q42315	Q42315 cyprinus ca
28	221	11.9	445	13 Q8841	Q8841 anguilla an
29	220.5	11.9	388	5 Q8MTW6	Q8MTW6 spisula sol
30	220	11.8	397	4 Q725R9	Q725R9 homo sapien
31	219.5	11.8	215	6 Q9GKP7	Q9GKP7 sus scrofa
32	219	11.8	470	11 P37842	P37842 rattus norv
33	218	11.7	394	5 Q9NHF3	Q9NHF3 aplysia cal
34	217	11.7	452	13 Q7T2S8	Q7T2S8 carassius a
35	216.5	11.7	346	6 Q95XS6	Q95XS6 ovis aries
36	216	11.6	460	5 Q8GME6	Q8GME6 caenorhabdi
37	215	11.6	331	13 Q801F3	Q801F3 fugu rubrip
38	214	11.5	385	4 Q86VF2	Q86VF2 homo sapien
39	214	11.5	559	11 Q9QW71	Q9QW71 rattus sp.
40	213.5	11.5	518	6 Q9MRT8	Q9MRT8 cryptotagus
41	212	11.4	394	5 Q9NJS6	Q9NJS6 aplysia kur
42	211.5	11.4	352	13 Q9YHY4	Q9YHY4 lampetra fl
43	211	11.4	445	13 Q98842	Q98842 anguilla an
44	210.5	11.3	459	11 Q8CGI5	Q8CGI5 mus musculu
45	210.5	11.3	515	11 Q9DBL0	Q9DBL0 mus musculu

ALIGNMENTS

RESULT 1

Q63004 PRELIMINARY; PRT; 438 AA.
ID Q63004
AC Q63004;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DE 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE 5-HT6 serotonin receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Striatum;
RX MEDLINE=96102917; PubMed=8522988;
RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RA Meltzer H.Y., Sibley D.R., Roth B.D., Hamblin M.W.;
RT "Cloning, characterization, and chromosomal localization of a human 5-
RT HT6 serotonin receptor."
RL J. Neurochem. 66:47-56(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 438 AA; 46786 MW; DB90403892F691A9 CRC64;

Query Match 13.5%; Score 250.5; DB 11; Length 438;
Best Local Similarity 24.7%; Pred. NO. 7e-13;
Matches 98; Conservative 69; Mismatches 176; Indels 53; Gaps 14;

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QY      2  GGEA-----LLAGLLVMVLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHL 53
      |||
      |||
Db     16  GPGPPPPAGGSGWAAALCVIVLTAANAASLLIVLICTQPAVENT--SNPFLVSLFTSDL 73
      |||
QY     54  LLAALDMPTFTLLGVMRGTPSAPGACGVIGPLDTFLASNAALSVAALSADOMLAVGFPRL 113
      |||
Db     74  MWGLVMPMPAMNLYGKRWVARGLCLLWTAFDVMCCSASILNLCISLDLYLLILSPRL 133
      |||
QY    114  YAGRL-PRRYAGLLIGCAWGOSLA-----FSGAALGCSWLGYSAFASCULRUPPEPRPR 168
      |||
Db    134  YKLRMTAPRALAILG-AW--SLAALASFLPLLIGMHELKART-----PAPGQCR 181
      |||
QY    169  FAA---FATLHVGCFVLPLAVLCITSLQVHRVARRHCQRMQDVT-----MKALLALA 218
      |||
Db    182  LLASLPFVLVVASGVTFPLPSGAICFTYCRILLAAARKQAVQVSLTGTGAQALETLQVPR 241
      |||
QY    219  DLHPSVR---QRCILQQRHRRHTRKIGIAITFLICFAPYVMFLAELVFPVTVNAQ 274
      |||
Db    242  TPRPGMESADSRRLAKTHSRKALKASITGLIGLGMFFVTLWLPFFVANIAQAVDCISPLG 301
      |||
QY    275  WGLSKCLTYSKAVADPTYSILRPPROVLGMV-----HLLKRTPRPASTHDS 326
      |||
Db    302  FDVLT-WLGYCNSVNPILYPLFMRDKRALGRFLPCVHCPPERASPASPMWTHSGA 360
      |||
QY    327  LDVAGMVHQLKRTPRPASTHNGSVDTENDSCLOOT 362
      |||
Db    361  R-PGLSLQVQLPLPLPPNSDSDSA-SGQTSGLQUT 393
      |||

RESULT 2
Q8QCG4 PRELIMINARY; PRT; 390 AA.
AC Q8QCG4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type five-like somatostatin receptor.
DS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoceratygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Peter R.E.;
RT "Cloning and expression of a type five-like somatostatin receptor in
RT goldfish.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY) .
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AP252879; AM18805.1;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR DR GO: GO:0004872; F:receptor activity; IEA.
DR DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR DR InterPro: IPR000276; GPCR Rhodops.
DR DR Pfam: IPR001092; HLH_Basic.
DR DR Pfam: PFO0001; 7tm1.1;
DR DR PRINTS: PR00237; GPCRHOODPSN.
DR DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR DR PROSITE: PS00282; G-PROTEIN_RECEP_F1_2; 1.
DR DR PROSITE: PS00038; HLH_1; 1.
DR DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-PROTEIN COUPLED RECEPTOR;
SQ SEQUENCE 390 AA; 44136 MW; EC12119AMB6CF9A8 CRC64;

Query Match 13.3%; Score 246.5; DB 13; Length 390;
Best Local Similarity 23.9%; Pred. No. 1.3e-12;
Matches 79; Conservative 59; Mismatches 122; Indels 71; Gaps 10;

QY      7  LLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLAALDMPFTLLG 66
      |||
Db     42  ILAVILVFWVLGNSLAIFVLYRYTKMT-ATNMYLNLVADELYLGLPFLTAH 99
      |||

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QY	67	VNRGTSAPGACQVIGFLDTFLASNAAISVAALSADQWLAVGFFPLRYAGRLRPVYAGLL	120
Db	100	NMLGWPFGFNELCRILMWTDSISQFTSTFCLTVNSIDRYMVAVHPPIRSARWRPRVAKVI	159
QY	127	LCGANGQSLSFGAALGCSWLGYSAFASCSLRLP	168
Db	160	NSWVA-----LSCLLTLPVIYCDVQPELNTCNLSWPEPRDVM	198
QY	169	FAAFATLHAGVGVPLAVLCLTSQVHRVARHCQRMQMTVTWKALALLADLHPSVQR	228
Db	199	STAFILYAMLGFFPFLMVICL-----CYLLIVIKVKSASARAGUS	239
QY	229	LQOKRRHRHTRKIGIAIATFLICAPYVMTRLAELVPPVTNA-QWGI--LSKCLTYS	285
Db	240	--KRGSEKKVTRMVIIVVVFVLCWLPFIINILNISLTPENSMTGFIYFVLITV	297
QY	286	KAVADPFYTSLL-----RRPFRQVLAGMVHRL	312
Db	298	NSCANPLLYSFLSDNFKRSFQVLC--IHKV	326
RESULT 3			
ID	Q9DQG6	PRELIMINARY; PRT; 380 AA.	
AC	Q9DQG6;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Somatostatin receptor type two.		
GN	SST2.		
OS	Carassius auratus (Goldfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Carassius.		
OX	NCBI_TaxID=7957;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	MEDLINE=20453044; PubMed=10996426;		
RX	Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;		
FT	"Molecular cloning and expression of a type-two somatostatin receptor		
RT	in goldfish brain and pituitary";		
RL	Mol. Cell. Endocrinol. 166:75-87(2000).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL; AF139597; AAF98367.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm1.1;		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.		
DR	PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.		
KW	G-protein coupled receptor, receptor, Transmembrane.		
SW	SEQUENCE 380 AA; 4316 MW; CB897FF7337CFA30 CRC64;		
Query Match 12.8%; Score 238.5; DB 13; Length 380;			
Best Local Similarity 24.1%; Pred. No. 6.1e-12;			
Matches 84; Conservative 63; Mismatches 163; Indels 39; Gaps 9			
QY	14	MYLAVALLSNALVILCCYASRLFRASGVLLVNLISLGHLLAALDMPFTLLGVNRGTP	73
Db	60	VWCAVGLCGNALVMVILRYAKOKT-VTNITILNLAVAD-VLCMLSPFTAIQLSLHWP	117
QY	74	SAPGACQVIGFLDTFLASNAAISVAALSADQWLAVGFFPLRYAGRLRPVYAGLLGCAWQ	133
Db	118	FGSAICRVVLTADSNMKNQFTSIFFLTWSDRYLAWVHPISKTKWKPMAKSIAMWVI	177
QY	134	SLAFSGAALGCSWLGYSAFASCSLRLLPPEPRPFAAFTATHAVGVPLAVLCLTSL	199
Db	178	SLVNLPIIMTYSVNVKKNKAEATCTMLMPEQNTYTVTFYTFMGFFFLIVICM---	234

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QY 194 QVHRVARRCQMDVTVMKALLADLHPSVRQCLIQKRRHRATRKIGIAIATFLIC 253
Db 235 -----CYLLIVIKVS-----SGNRVSSKGRKSRKVTMRVMSVVVFLC 276
QY 254 FAPYV---MTRLAELVPFVTVNAQWILSKCLITYSKAVADPTYSLL-----RRPRQVLA 306
Db 277 WLPFFVFNVTSGTPTVPLKSTDFVVLVIGYANSCANPILYAFSLDNFKKSFQNVLC 336
QY 307 GMVHRLKTRP--RPASTHSDSLDVAGMVHOLLKTRPRPASTHNGSVDT 353
Db 337 -----LKRUGLDEIERSDSRQDRTRMVDVMSSET-HNAALLNGDLQT 378

RESULT 4
Q8UWL5 PRELIMINARY; PRT; 370 AA.
AC Q8UWL5, 01-JUN-2003 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Somatostatin receptor 2.
GN SSTR2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=21564205; PubMed=11707075;
RX Bagheri-Fam S., Ferraz C., Demalle J., Scherer G., Pfeifer D.;
RA "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:
RT Conservation of Short Regulatory Sequence Elements within Large
RT Intergenic Regions."
RL Genomics 78:73-82(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF329945; AAJ32173.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 370 AA; 41364 MW; 420BB12F204946B6 CRC64;

Query Match 12.8%; Score 237; DB 13; Length 370;
Best Local Similarity 22.9%; Pred.No. 7.9e-12;
Matches 86; Conservative 61; Mismatches 133; Indels 96; Gaps 14;

QY 14 MVLAVALLSNALLCCAYSAELTRASGVLLVNLISGLHLLAALDMPFTLLGVRGTRP 73
Db 53 LVCAVGLGNAIVYILRYAKMKT-VTHYIILNLAADVLP-MLGLPIAQLALVHP 110
QY 74 SAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFLPRYAGRLRPVYAGLLGCGAQ 133
Db 111 FGPVLGRVMTVDLSLQKFTSIFCLAVMSIDRYLAVVHPKTKWRKPRVAKTINVAVNGA 170
QY 134 SLA-----FSGAAL--GCSWLGYSSAFASGLRLPPEPRPFAATLHAGVFL 183
Db 171 SLVNVLPVIVYSGLIIPKQDC-----FCTI-VWPEPEAYTAFMYTFLIGFL 219
QY 184 PLAVLCITSLQVHRVARRHCQMDVTVMKALLADLHPSVRQCLIQKRRHRATRKI 243
Db 220 PLLVISL-----CYVPIIVKVKSSGIRVGSS-----KKRGRKRVTRMV 258
QY 244 GIAIAFLICFAPYVMTRLAELV-----PFVTVNAQWILSKCLITYSKAVAD 290

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Db 259 SIIVAVFVLCWLPFYVFNVTSGTGS:SATHVLRSTFAFVV-----LGVANSCAN 308
QY 291 PFTYSLRLRRPR-----QVLGVMVHLLKRTPRPASTHSDSLDVAGMVHOLLKTRP 341
Db 309 PILYAFISENFKSFQNVLCGLQKVGL-----DEAERSDSRQDKSRMIND----- 353
QY 342 RPASTH-----NGSVDT 353
Db 354 -PTETRSTLLNGDLQT 368

RESULT 5
Q86ME4 PRELIMINARY; PRT; 399 AA.
AC Q86ME4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein F15A8.5.
GN F15A8.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
[2]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC STRAIN=Bristol N2;
RA Miller N.;
RT "The sequence of C. elegans cosmid F15A8."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Waterston R.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; U97549; AA091738.1; -.
DR WormPep; F15A8.5c; CE33617.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000412; ABC_transport2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00890; ABC2_MEMBRANE; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW Hypothetical protein
SQ SEQUENCE 399 AA; 45526 MW; 40629EF6E074D048 CRC64;

Query Match 12.8%; Score 237; DB 5; Length 399;
Best Local Similarity 23.2%; Pred.No. 8.6e-12;
Matches 82; Conservative 61; Mismatches 142; Indels 68; Gaps 11;

QY 8 LAGLLVAVALLSNALLCCAYSAELTRASGVLLVNLISGLHLLAALDMPFTLLGV 67
Db 8 LLGFLSVLITIALFGLNLLVCAAILNDRSLRKQENFLVSLAVSDLLVSVLWMLFAVND 67
QY 68 MRGTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFP---LRVAGRLRPYAG 124
Db 68 ILGWPFQGFQVCFWISFDITTCATSLINLCALSLDRYWHISRPMVYIRYCNRRINVI 127

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QY 125 LLLGCWAGSLAFSGAALGCSWLGYS--AFASCSLRLLPPEPRFAAFTATL 176
DB 128 VLV---WLISAGIAGAPLG---FGFGSKVTINNLTLGLPVCERLP-----LPYAIGS 173
QY 177 HAVGVFLPLAVLCLTSLQVHRVARHRCORMDVTWKALALL-----ADLHPSVRQR 227
DB 174 SMVSFPLPAMVILYTKLYLARKHRSIKTQLQCATSFILMQASEKIREIRTSIFS 233
QY 228 -----CLIOQKRR-----HRAIRKIGIAIATPLICFAPYVMT----- 261
DB 234 LNFLCPTFRKQNSQDPHTPAHNRNSISDQKARLTGLVINGTLVCLWLPFFFTVNLRA 293
QY 262 -LAELVPFVTVNA-OWGILSKCLTYSKAVADPFTYSLRRPFRQVLAMVHRL 312
DB 294 WLPEIFSSKTIIVATW-----LGYANSSANPLIYSIFNRDFFRAFKKIIVRV 340

RESULT 6
Q86ME5 PRELIMINARY; PRT; 402 AA.
AC Q86ME5;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein F15A8.5.
GN F15A8.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RT "The sequence of C. elegans cosmid F15A8."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97549; AA091737.1; -.
DR WormPeP; F15A8.5b; CE33616.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000412; ABC transp2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00890; ABC2 MEMBRANE; 1.
DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR_F1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 45856 MW; 06ABE42C0970CBF5 CRC64;

Query Match 12.8%; Score 237; DB 5; Length 402;
Best Local Similarity 23.2%; Pred. No. 8.7e-12;
Matches 82; Conservative 61; Mismatches 142; Indels 69; Gaps 11;

QY 8 LAGLVNVLAVALLSNALVLLCCVSAELRTRASGVLLVNLGLHLLAALDMPFTLLGV 67

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DB 8 LLGLFSLVLIILFGLNLCVCAAILWDRSLRKQENFLVSLAVSDLLVSLVLMFAAVND 67
QY 68 MRGRTSAPCAQVIGFLDTFLASNAALSVAALSADQWLAVGFP-----LRYAGRLRPRYAG 124
DB 68 ILGWYFGQFYCFQWISFDITTCASILNLCALSDRYWHISRPMWYIRYCNRRIRNYVI 127
QY 125 LLLGCWAGSLAFSGAALGCSWLGYS--AFASCSLRLLPPEPRFAAFTATL 176
DB 128 VLV---WLISAGIAGAPLG---FGFGSKVTINNLTLGLPVCERLP-----LPYAIGS 173
QY 177 HAVGVFLPLAVLCLTSLQVHRVARHRCORMDVTWKALALL-----ADLHPSVRQR 227
DB 174 SMVSFPLPAMVILYTKLYLARKHRSIKTQLQCATSFILMQASEKIREIRTSIFS 233
QY 228 -----CLIOQKRR-----HRAIRKIGIAIATPLICFAPYVMT----- 261
DB 234 LNFLCPTFRKQNSQDPHTPAHNRNSISDQKARLTGLVINGTLVCLWLPFFFTVNLRA 293
QY 262 -LAELVPFVTVNA-OWGILSKCLTYSKAVADPFTYSLRRPFRQVLAMVHRL 312
DB 294 WLPEIFSSKTIIVATW-----LGYANSSANPLIYSIFNRDFFRAFKKIIVRV 340

RESULT 7
Q8BLD9 PRELIMINARY; PRT; 478 AA.
AC Q8BLD9;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE D.
GN DRD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK045456; BAC32378.1; -.
RL PIR; PT0721; PT0721.
RL MGD; MGI:94927; Drd5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR_F1_2; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR_F1_2; 1.
SQ SEQUENCE 478 AA; 53076 MW; D391658C55813DF CRC64;

Query Match 12.5%; Score 233; DB 11; Length 478;
Best Local Similarity 22.9%; Pred. No. 2.3e-11;
Matches 82; Conservative 76; Mismatches 146; Indels 54; Gaps 13;

QY 1 MGCEALLAGLVNVLAVALLSNALVLLCCVSAELRTRASGVLLVNLGLHLLAALD 60
DB 34 LGPAQVVTAGLLTLLVILLGNLVCAIVRSRHLRAKWTNIFIVSLAVSDFVALLVM 93
QY 61 PFTLLGVNMRGRTSPAPCA-QVIGFLDTFLASNAALSVAALSADQWLAVGFPYRAGR 119
DB 94 PKRAVAEVAGYVWF--GAFCDIWWAFDIMCSTASILNLCIISVDRYWALSRRPRYERKMT 151
QY 120 PRVAGLLGCWAGSLAFSGAALGCSW---LGYSSAFASCSLRLLPPE----- 163

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Db 152 QVALVWVALAWTSLISLIPVQLNWRDKAGSQREGLLSNLTPWEEGWELDQRTENC 211
QY 164 -PERPFAAFTATLHVGVLPLAVLCLTSLOVHRVAREHRCORMDVTVMKALLADLHP 222
Db 212 DLSLNTYAISSLS--ISYIPVIMVITYIYRIAQVQIRR-----ISSLERAEHQA 264
QY 223 SVQR-----CLIOQKRRHRATKIGIAIATFICFAPYVMTLAEVLVFTVNAQM 275
Db 265 SCRSRGACEPDPPLSRASIKETKVFRTLSVINGVFVCCWLPFFI--LNCMVFPFCSSGDAQ 322
QY 276 GILS--KCLT-----YSKAVADPFTYSL--LRPFRQVLGVMVHLLKRT 317
Db 323 GPTGFPVSEITFDIFVWFGWANSLSNPIIAFNAADPKVFAQLL-GCSH-LCFTPT 378

RESULT 8
Q9YH3 PRELIMINARY; PRT; 353 AA.
AC Q9YH3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Putative odorant receptor LOR4.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory organ;
RA Berghard A., Dryer L.;
RT "A novel family of ancient vertebrate odorant receptors.";
RL J. Neurobiol. 0:0-0(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF069547; AAC82382.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR EMBL; AF070289; AAL50221.1; -.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR PROSITE; PS00038; HLH 1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 353 AA; 39501 MW; D89F8D6FC627180 CRC64;

Query Match 12.5%; Score 231.5; DB 13; Length 353;
Best Local Similarity 22.0%; Pred. No. 2.2e-11;
Matches 76; Conservative 88; Mismatches 147; Indels 35; Gaps 10;

QY 1 MGGEALLAGLVWVLAVALLSNALVLLCCAYSALRTRASGVLLVNLGLHLLAALDM 60
Db 28 MSRTAALSATITLILA-TVLGNLLIITSIAVPRQLQTR-TNIALSLAVADLVGLVTVM 85
QY 61 PFTLLGWGRTPSAPCAQVIGLDTFLASNAALSVLAALSDQMLAVGFPLRYAGRLRP 120
Db 86 PYSMMKAVYKCFYGOFFCNQLQVFLDYMLTNSIMHLGCIADRYVAICDPLRYQRTVN 145
QY 121 RVAGLLGCGAWGSLAFSGAALGCSWLGYSFASCSLRLPPEPRPFAATATLHVG 180
Db 146 HTVVTWLLISWFGPALFSSPIL-----VNFNPMSRGNIEIISCPNQCLFVSTWLVSVVG 201
QY 181 ---FVLPLAVLCLTSLOVHRVAREHRCORMDVTVMKALLADLHPSVQR-----CLIQ 231
Db 202 VCPYVLSLITMSVYARIIVARQRISSVLSQ-----VHAQOQQOQQAFTNIR 254
QY 232 QK-----RRHRATRKIGIAIATFICFAPYVMTLAEVLVFTVNAQMGLSKCLTYSKA 287
Db 255 QKWAMKREHSAKTLGSIIGVYLLSWLPFYMVL--PPFPNQSSAAVRITTWIGYISS 312

QY 288 VADPFTYSLRRPPRQVLGVMH-RLIKRTRPASTHDSLSLDVAGM 332
Db 313 AINPVLVATLNRPPSAFVAISKVL-----SSTRATMDLSGV 352

RESULT 9

Q9HBV6 PRELIMINARY; PRT; 425 AA.
AC Q9HBV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypocretin receptor-1.
GN HCRTR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20429525; PubMed=10973318;
RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
RA Nevimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
RT "A mutation in a case of early onset narcolepsy and a generalized
absence of hypocretin peptides in human narcoleptic brains.";
RL Nat. Med. 6:991-997(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yeager M., Welch R., Haque K., Bergen A.;
RT "Genomic sequence of the hypocretin (orexin) receptor 1 (HCRTR1).";
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580342; PubMed=11723285;
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA Stefansson K., Gulcher J.R.;
RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL Neurology 57:1896-1899(2001).
DR EMBL; AF202084; AAG28020.1; -.
DR EMBL; AF202078; AAG28020.1; JOINED.
DR EMBL; AF202079; AAG28020.1; JOINED.
DR EMBL; AF202080; AAG28020.1; JOINED.
DR EMBL; AF202081; AAG28020.1; JOINED.
DR EMBL; AF202082; AAG28020.1; JOINED.
DR EMBL; AF202083; AAG28020.1; JOINED.
DR EMBL; AF070289; AAL50221.1; -.
DR EMBL; AY062030; AAL47214.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016499; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR04059; Orexin_receptor1.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01521; OREXIN1R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
KW Receptor.
SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 12.4%; Score 230.5; DB 4; Length 425;
Best Local Similarity 25.3%; Pred. No. 3.3e-11;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

QY 5 EALLAGLVWVLAVALLSNALVLLCCAYSALRTRASGVLLVNLGLHLLAALDMPTFL 64
Db 46 EWLIIAAVAVFVYVAVLGVNTLVCLAVWRNHRMT-VTNYFVNLSLADLVITACIPASL 104

QY 65 LGVNRGRTPSPAGCQVIGFDTFLASNAALSVAAALSDQWLAVGFFLRVAGRLRPRYAG 124
 Db 105 LVDITESWLFCHALCKVPIYQAVSVAVITLSFIALDRWYALCHELLPKSTAR-RARG 163
 QY 125 LLLCANGOSLAFSGAALGCSWLGYSSAFASCSLRLEPPEPRFAA-----FTA 174
 Db 164 SILG-IWAVSLAI-----WVFOAAVMECSVLPELANRKLFSVCDERWADDLYPK 213
 QY 175 TLHVGFLP-LAVCLTSLQVHRVARRHCQMDVTVMKALA-----LLADL----- 220
 Db 214 IYHSCFFIVTVALPLGMAWAFQIFRKLNGRQIPGTTLSALVRNWKRPQDLGDLQGLS 273
 QY 221 HPSVRQCL---IQQRHRRATRKIGIALAFLICFAP-----YVTRLA--- 263
 Db 274 GEPQFRARAFLEVKOMRARKTKAKMLVMVLLNFALCYLPISVLNVLKRVFGMFRQASDR 333
 QY 264 ELVPEFTVNAOGLSKCLTYSKAVADPFTYSLRRRFRQVL-----AGMVERLL 313
 Db 334 EAVYACTFESH-----LVYNSAANPIIYNFLSGKFRQKAAFSCLPLGLGPCGSLK 387
 QY 314 KRTPRPASTHDS 325
 Db 388 APSRSSASHKS 399

RESULT 10

Q8MI04 PRELIMINARY; PRT; 367 AA.
 AC Q8MI04;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Somatostatin receptor subtype 5.
 GN SS15.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RA Debus N., Dutoir A., Boudouresque F., Vuaroqueaux V., Oliver C.,
 RA Ouafik L.;
 RT "Molecular cloning and tissue distribution of the ovine somatostatin
 RT receptor subtype 5: osst5";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RA Debus N.;
 RT "Regulation of GH secretion in sheep: Role of somatostatin and its
 RT receptors";
 RL Thesis (1999).
 RL Department of Interdisciplinary communications in Endocrinology,
 RL University of Aix-Marseille II, Marseilles, France.
 DR EMBL; AJ441116; CAD9615.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR University of Aix-Marseille II, Marseilles, France.
 DR EMBL; AJ441116; CAD9615.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 KW Receptor.
 FT CHAIN 2 367 SOMATOSTATIN RECEPTOR SUBTYPE 5.
 SQ SEQUENCE 367 AA; 40269 MW; FASCA87A8ABED764 CRC64;
 Query Match 12.4%; Score 230; DB 6; Length 367;
 Best Local Similarity 26.2%; Pred. No. 3.1e-11;
 Matches 79; Conservative 51; Mismatches 138; Indels 34; Gaps 8;

QY 11 LILVMVALLSNALVILCCAYSAELRTRASGVLLVNLSLGHLILAALDMPTLLGVNRG 70
 Db 46 LYLVCVAGLGGALVIVVLRHAKMT-VTNVILNLAADVLL-MGLSPFVATQNAIS 103
 QY 71 RTPSPAGCQVIGFDTFLASNAALSVAAALSDQWLAVGFFLRVAGRLRPRYAGLLGCA 130
 Db 104 YWPFGEVLCRLVMTLDGNGQFTSIFCLTVMSVDRLVAVVHFIARWRPRPVAKLASAAV 163
 QY 131 MQOSLAFSGAALGCSWLGYSSAFASCSLRLEPPEPRFAAFTATLHAGVFLPLAVLCL 190
 Db 164 NAFSLVMSLPLV--VFADIQEGWNTCNLTW-PEPVGLMGAVFIITYTSVLGFFGLLVICL 220
 QY 191 TSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKKRRHRATKIGIAIATF 250
 Db 221 -----CYVLIVVVKLKASGV-----RVGSTRRSERKVTMVRVVVLVF 258
 QY 251 LTICFAPYVMTLAEI---VPFVTVNAOGLSKCLTYSKAVADPFTYSL-----LRPRFQ 303
 Db 259 AGCMLPFFIVNVLNLAFLPALPEPASAGLYPFVVLVSYANSCANPCLYGLSDNLRQSPRK 318
 QY 304 VL 305
 Db 319 VL 320

RESULT 11

Q9YHY2 PRELIMINARY; PRT; 340 AA.
 AC Q9YHY2;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Putative odorant receptor LOR14.
 OS Lampetra fluviatilis (River lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzoniformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7748;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory organ;
 RA Berghard A., Dryer L.;
 RT "A novel family of ancient vertebrate odorant receptors.";
 RL J. Neurobiol. 0:0-0(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF069548; AAC82383.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 340 AA; 37947 MW; E329864C73C18F25 CRC64;
 Query Match 12.4%; Score 229.5; DB 13; Length 340;
 Best Local Similarity 22.2%; Pred. No. 3.1e-11;
 Matches 74; Conservative 65; Mismatches 141; Indels 53; Gaps 9;

QY 2 GPCEALLAGLLVMV-----LAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLGHLILA 56
 Db 23 GPTQVREVRVLLVITVFAFITATILNLLIITAIASFKYKLTQTHAN-FLAISLAVSDLLVG 81
 QY 57 ALDMPFTLLGVNRGRTPSPAGCQVIGFDTFLASNAALSVAAALSDQWLAVGFFLRVAG 116
 Db 82 VFTMPLSMVKTYVDCWVYASVLCNARYFLDYTLTTATILHITCIADRYVAICDELRYAT 141
 QY 117 RLRPVAGLLGANGQSOLFASGALGCSWLGYSSAFASCSLRLEPPEPRFAAFTATL 176
 Query Match 12.4%; Score 230; DB 6; Length 367;
 Best Local Similarity 26.2%; Pred. No. 3.1e-11;
 Matches 79; Conservative 51; Mismatches 138; Indels 34; Gaps 8;

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Db 142 RVTETIAALLVLCWGAIFSSPIL-----LSFSTLSRGNIERASCDDCVFVSFGIL 197
QY 177 HAUG---FVLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQCLIQOK 233
Db 198 VTIVGPGPFTAHVVLVAVYIVVARQSRKV-----AADSSAVKQM 240
QY 234 RRRHRAIRKIGIAITFLICFAPYWTBLAE-----LVPFVTVNAQWGLSKCLTYSKA 287
Db 241 KREHSAAKTLGAILGTFMLSPLYVVVAMGFTVDGLFIPYRV--AMW-----IGYCSS 292
QY 288 VADPPTYSLRRPPR-----OVLAGMVHR 311
Db 293 AINPLLYASFNPFTATFDIFELRVFSGVVR 325

RESULT 12
Q9JK40
ID Q9JK40 PRELIMINARY; PRT; 385 AA.
AC Q9JK40;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Somatostatin subtype 5 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA O'Carroll A.-M.;
RT "Cloning, sequence and tissue distribution of the gene encoding a
RT mouse somatostatin subtype 5 receptor."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF268067; AAF72547.1; -.
DR HSSP; P02699; 1F88.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 385 AA; 42489 MW; 58C1140BF09FCEB5 CRC64;

Query Match 12.3%; Score 229; DB 11; Length 385;
Best Local Similarity 25.7%; Pred. No. 3.9e-11;
Matches 95; Conservative 53; Mismatches 162; Indels 60; Gaps 13;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
Db 56 MGAARVLPVLYLVCTVGLGNTLVITVVRVYAKMT-VTVNLMLNADVADLVF-MGL 113
QY 61 PFTLLGVNRGRTSPAGCAQVIGFDLTFASNAALSVAALSADQWLAVGFPLRYAGLRP 120
Db 114 PFLATQNAVSVYVPGSFCLRWLTLDGINQFTSFCLMWVSDRYLAVVHPLRSARWRP 173
QY 121 RYAGLLGCANGOSLAFSGAALGCSWLGYSAPFASCSLRLLPPEPRPFAAFTALHVG 180
Db 174 RVAKLASAAVWVFLMLSLPLL--VFADVQBGWGTGNLSW-PEPVGLWGAFTITYTVLG 230
QY 181 FVLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQCLIQOKRRHRAT 240
Db 231 FFGPLLVLCL-----CVLLIVVKYKAGMRV-----SSRR-----RSEKVT 269
QY 241 RKIGIAITFLICFAPYWTBLAE-----LVPFVTVNAQWGLSKCLTYSKAVADPFTYSL 297
Db 270 RMVTVVVLVFGVGLPFPFIVNVNLAFTLPEPTSAGLYFFVVVLSVANSANPLLYGFL 329
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QY 298 ----RRPFRQVLAGMVHRLKR-----TPRPASTHSDSLDVAGMVHQLKRTPRP 343
Db 330 SDNFRQSRKALC-----LRGQGVEDADALEPR-----DKSGRPQTTL-----PTR 372
QY 344 ASTHNGSVDT 353
Db 373 SCEANGLMQT 382

RESULT 13
O42316
ID O42316 PRELIMINARY; PRT; 437 AA.
AC O42316;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE DIA4 dopamine receptor.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=99044151; PubMed=9826915;
RA Hirano J., Archer S.N., Djamgoz M.B.A.;
RT "Dopamine receptor subtypes expressed in vertebrate (carp and eel)
RT retinae: cloning, sequencing and comparison of five D1-like and three
RT D2-like receptors."
RL Recept. Channels 5:387-404 (1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Y14627; CA94971.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 437 AA; 48707 MW; A44749475E2139CE CRC64;

Query Match 12.3%; Score 228.5; DB 13; Length 437;
Best Local Similarity 22.3%; Pred. No. 4.9e-11;
Matches 74; Conservative 79; Mismatches 142; Indels 37; Gaps 13;

QY 7 LLAG-LLVMVLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDMPTILL 65
Db 22 VLTGCFLSLLITLLTGLNLTLCVCAAVTKPHLRASKVTNFFVISLAISDLVAVLWPMKAA 81
QY 66 GVMRGTEPSAPCA-QVIGFDLTFASNAALSVAALSADQWLAVGFPLRYAGLRPRVAG 124
Db 82 SEIVGFWFPF--GAFCDVWVAFDMCSTAILNLCVISVDRYWAISSPFYERKMTPKVAF 139
QY 125 LLLGCANGOSLAFSGAALGCSWLGYSAPFASCSLRLLP-----EPERPFAAFTALHVG 181
Db 140 IMLSLAWTSLISLIPVQLNWHKQAQELNGTYGELPDNCDSSLNRYTVAISSSL--ISF 197
QY 182 VLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQCLIQOK-----R 234
Db 198 YIPVAILMVTYTRIYIAQKQIRISALE-RAAESAKNRHSHSMGNMNASWESSSEFSGFK 256
QY 235 RRHRAIRKIGIAITFLICFAPYWTBLAEVLPFVTVNAQWGLSKCLT----- 283
Db 257 RETKVLKLSVTVGVCWLPFFV--LNCWVPFCNPNE--GSDFFCISSTTFDFVWVG 312
QY 284 YSKAVADPFTYSL-----LRRPFRQVLAGMVHRL 312
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Db 313 WANSLSNPIIYAFNAGFRKAP-SILIG-CHRL 342

RESULT 14

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O9PVGO PRELIMINARY; PRT; 367 AA.
ID Q9PVGO
AC Q9PVGO
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Somatostatin receptor type 1 subtype A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2000543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
RL receptors in goldfish brain."
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF097726; AF09813.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41658 MW; BE85E6C26C103614 CRC64;

Query Match 12.28; Score 227.5; DB 13; Length 367;
Best Local Similarity 23.04; Pred. No. 5e-11;
Matches 86; Conservative 75; Mismatches 160; Indels 53; Gaps 14;

QY 2 GPGEALAGLVLMVAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMP 61
Db 31 GSSAIFISFYVVLGLGNSWIVVIERAKMT-ATNIYILNLAIDELL-MSVP 88
QY 62 FTLLGVNRGTPAGACQVIGFIDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP 121
Db 89 FLVTSLLHHWPGSLLCRLVSLVDAINMFTSYICLTVLSDIRYISVHPHKAARYRRPT 148
QY 122 YAGLLGCAMGQS-----LAFSGAALGCSWLGYSAFASCSRLRPPPERPFAAFTA 174
Db 149 IAKVNLGVWVFSILVILPIIISTAPN-----SDGSVACNMQM-PEPERQWMAVFI 201
QY 175 TLHAGVFLPLAVLCFSLQVHRVARHRCQMDVTVMKALLADLHPSVQRCLIQQR 234
Db 202 YAFLMGFLFPVIAICM-----CYILLIIVKRVVVALKAGNQ-----QRKK 240
QY 235 RHPRATKIGIAIATATLFCFAPYVMTLAEIVPFTV-NAQWGLSKCLTYSKAVADPFT 293
Db 241 SERKITLWVMVVTVFVCMWPHMGVSV-FVQHNATLSQLAVILGYANSCANPIL 298
QY 294 YSLI-----RRPFRQVLAGMVRHLKRTPRPASTHDSLDVAG-MVHQLKRTPRPASTN 348
Db 299 YGFLSDNFRSFRILC-LRWMDNATEEPIDYATALKSRGYSVDDF-----OPENLES 351
QY 349 GSDVTENDSCLQQT 362
Db 352 GST-YRNGTCTST 364

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RESULT 15

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O96716 PRELIMINARY; PRT; 391 AA.
AC O96716
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine D1/beta receptor.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardinaud B., Gilbert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA Vincent J.D., Niznik H.B., Vernier P.;
RT "The amphioxus D1/beta receptor and the emergence of the vertebrate
RL adrenergic system."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ005433; CA06536.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 42622 MW; 67A5AD944AFA3FBE CRC64;

Query Match 12.28; Score 227.5; DB 5; Length 391;
Best Local Similarity 20.98; Pred. No. 5.3e-11;
Matches 77; Conservative 80; Mismatches 159; Indels 53; Gaps 12;

QY 5 BALLAGLLVMVAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPFTL 64
Db 39 QAVLGITVILLITVIGNVILAVTCHRMRT-VTNFFIVSLACADLSVGITVLPFAA 97
QY 65 LGVMRGRTSPAGACQVIGFIDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRPYAG 124
Db 98 TNDILGVWVFG-GYCDVWVSFDVNLNSTASILNVLVIAFDRLAITAPFTYHTRWERTAG 156
QY 125 LLLGCAMGQSALFSGAALGCSWLGYSAFASCSRLRPPPERPFRF---AAFTATLHAGVF 181
Db 157 ILIATVWGISLVWSFLPIQGW--YRDNQSEALAIYSDPCLCIFTASTAYTIVSSLSIF 214
QY 182 VLPLAVLCFSLQVHRVARHRCQMDVTVMKALLADLHPSVQRCLIQQR----- 236
Db 215 YIPLILMLVFYGIIFKAARDQARKINALEGR-----LQENNRGKKIS 257
QY 237 ---HRATRKIGIAIATLFCFAPYVMTLAE-----LVFPFTVNAQW-GILSKCLTY 285
Db 258 LAKEKAAKTGIIMGVFILLCMFPFVNVINVPFCDCVQPAVEIALTWLGWINSCE--- 314
QY 286 KAVADPFTYSLRPPRQVLAGV--HRLKRTPRPASTHDSLDVAGMVRHQLKRTPRP 343
Db 315 ---NPIIYA-FNKEFRKVFVKMICCHKRGVTVGP---NHADLNYPFVAMRLKRGENA 366
QY 344 ASTHNGSV 352
Db 367 NGTVNGDAN 375

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Search completed: May 18, 2004, 12:08:08

Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:06:02 ; Search time 22 Seconds
(without alignments)
851.829 Million cell updates/sec

Title: US-10-049-569-2
Perfect score: 1858
Sequence: 1 MGPGEALLGLVMYLAVAL.....ASTHNGSVDTENDSCLQOTH 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	848	45.6	337	2	US-09-013-634-2
2	236	12.7	348	3	US-08-875-540-13
3	236	12.7	348	4	US-09-171-456-17
4	236	12.7	348	4	US-09-473-634-13
5	232.5	12.5	359	2	US-08-748-485-5
6	232.5	12.5	391	3	US-08-120-601B-8
7	230.5	12.4	402	1	US-08-444-734A-6
8	230.5	12.4	402	1	US-08-087-772A-15
9	230.5	12.4	402	3	US-08-846-704-4
10	230.5	12.4	408	1	US-07-916-901-2
11	230.5	12.4	408	3	US-08-450-962-2
12	230.5	12.4	408	3	US-08-450-962-5
13	230.5	12.4	408	4	US-08-848-631-2
14	230.5	12.4	408	4	US-08-848-631-5
15	230.5	12.4	425	4	US-09-479-128-2
16	229.5	12.4	402	4	US-08-462-509B-2
17	229.5	12.4	402	5	PCT-US95-05616-2
18	229.5	12.4	425	3	US-08-846-704-2
19	229.5	12.4	425	4	US-09-211-823C-22
20	228.5	12.3	391	1	US-07-816-283-2
21	228.5	12.3	391	1	US-07-816-283-4
22	228.5	12.3	391	1	US-08-417-103-2
23	228.5	12.3	391	1	US-08-417-103-4
24	228.5	12.3	391	1	US-08-417-103-14
25	228.5	12.3	477	1	US-07-791-936A-2
26	228.5	12.3	477	1	US-08-383-781B-2
27	228.5	12.3	477	2	US-07-969-267B-2

28	228.5	12.3	477	4	US-09-168-510-2	Sequence 2, Appli
29	228	12.3	385	4	US-08-981-700A-4	Sequence 4, Appli
30	228	12.3	387	3	US-08-993-088A-7	Sequence 7, Appli
31	228	12.3	387	4	US-08-993-424B-7	Sequence 7, Appli
32	228	12.3	387	4	US-09-595-549-10	Sequence 10, Appli
33	228	12.3	387	4	US-09-603-680-7	Sequence 7, Appli
34	228	12.3	387	4	US-08-899-112B-28	Sequence 28, Appli
35	228	12.3	475	1	US-07-686-591-4	Sequence 4, Appli
36	228	12.3	475	1	US-07-970-715-4	Sequence 4, Appli
37	227.5	12.2	408	1	US-08-351-473B-3	Sequence 3, Appli
38	226.5	12.2	359	2	US-08-103-170-4	Sequence 4, Appli
39	226.5	12.2	359	2	US-08-103-170-6	Sequence 6, Appli
40	226.5	12.2	400	2	US-08-103-170-9	Sequence 9, Appli
41	226	12.2	353	2	US-08-467-559B-10	Sequence 10, Appli
42	225.5	12.1	365	2	US-08-428-243-9	Sequence 9, Appli
43	225.5	12.1	365	5	PCT-US93-10301-9	Sequence 9, Appli
44	224	12.1	369	3	US-08-120-601B-9	Sequence 9, Appli
45	224	12.1	372	2	US-08-626-685A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-013-634-2
; Sequence 7, Application US/08991946A
; Patent No. 5945306
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Tang, Tom Y.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.946A
; FILING DATE: December 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0445 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; Sequence 2, Application US/09013634
; Patent No. 5945307
; GENERAL INFORMATION:
; APPLICANT: M. Alexandra Glucksmann and Keith Robison

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; TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,634
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Attorney, Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MWI-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-634-2

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Query Match 45.6%; Score 848; DB 2; Length 337;
Best Local Similarity 52.0%; Pred. No. 9.6e-66;
Matches 170; Conservative 52; Mismatches 101; Indels 4; Gaps 1;

QY 1 MCGEALLAGLVVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MNSWDAGLAGLVGTGVSLSNALVLLCLLHSDIRQAPALTEMLNGLCTVNM 60
QY 61 PFTLLGVNMGRTSPAGCAQVIGFDTFLASNAALSVAALSDOWLAVGPFPLRYAGRLRP 120
DB 61 PLTLAGVVARQPGADRLCLRAAFDLTFLAANSMLSAALSIDRWAVVFPPLSYRAXRL 120
QY 121 RVAGLLGCAGCQSLAFSGAALGCSWLGYSYSAFASCSRLPPEPRPFAAFTATLHVG 180
DB 121 RDAALMVAYTWLHALTTPAALALSGLFHQYASCTLCSSRRPDERLURFAVFTGAFHALS 180
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DB 181 FLLSFVNLCTYLVKLVARFCKRIDVTWTLVLLVDLHPSVRERCLBEQKERRQAT 240
QY 241 RKIGIAITFLICFAPYVMTLAEVFPVTVNAQWGLSKCLTYSKAVADPFTYLLRRP 300
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QY 301 FQVLGAGVHRLKTRTPASTHDSLL 327
DB 301 YNKSCKEILNRLHR-----RSIHSSGL 323

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RESULT 2
US-08-875-540-13
; Sequence 13, Application US/08875540A
; Patent No. 6015888
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan

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; APPLICANT: Wright, Simon Ralph
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; TITLE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/08/875,540A
; CURRENT FILING DATE: 1998-01-05
; EARLIER APPLICATION NUMBER: PCT/EP96/00397
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: GB9503866.7
; EARLIER FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO.13
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-875-540-13

```

```

Query Match 12.7%; Score 236; DB 3; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;

QY 12 LVMVLAVALL-----SNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPTLLGV 67
DB 18 ITVLAVALIITVAGNVVYVCLAVGLNRRLR-NLTNCFIVSLAITDLGLGLVLPFSAIYQ 76
QY 68 MEGRTSPAGCAQVIGFDTFLASNAALSVAALSDOWLAVGPFPLRYAGRLRPYAGLLL 127
DB 77 LSKWISFGKVCNIYVTSLDVMLCTASILNLFMSIDRYCAVMDPLRYPVIVTPARVAISL 136
QY 128 GCAGCQSLAFSGAALGCSWLGYSY-----APASGLRLPPEPRPFAAFTATLHVG 181
DB 137 VLIWVISITLSFLSIHLGWSNRNETSKGNHTTSKCNQVN-----EYGLVDGLVTF 188
QY 182 VLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQRCCLIOQKRRHRAT 241
DB 189 YLPLIMCITYYRIFRVARDOQAKRIDHISWKAAT-----REHRAV 231
QY 242 KIGIAITFLICFAPYVMTLAEVFPV-----TVNAQWGLSKCLTYSKAVADPFT 293
DB 232 TLAAYVGAFLICWFPY-----FTAFVYVGLRGDDAINEMLEAIVLWLGYSANALNPIL 284
QY 294 YSLLRPPR---OVLGAGVHRLKTRTPASTHDSLL-DVAGMVHQLKTRTP 342
DB 285 YAALNRDFTGYCQL--FCCLANR-----NSHKTSLRSNASQLSRTQSREPR 330

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RESULT 3
US-09-171-456-17
; Sequence 17, Application US/09171456A
; Patent No. 6346380
; GENERAL INFORMATION:
; APPLICANT: Wright, Simon Ralph
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; TITLE OF INVENTION: DETECTION OF VARIATIONS IN HUMAN H2 RECEPTORS
; FILE REFERENCE: 09347/004001
; CURRENT APPLICATION NUMBER: US/09/171,456A
; CURRENT FILING DATE: 1999-08-03
; EARLIER APPLICATION NUMBER: PCT/GB97/01075
; EARLIER FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO.17
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-171-456-17

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Query Match 12.7%; Score 236; DB 4; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;

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QY 12 LVNVLAVALL----SNALVLLCCAYSABLRTRASGVLLVNLISGLHLLAALDMPFTLLGV 67
Db 18 ITVVLAVLITITVAGNVVCLAVGLNRRLR-NTNCFIVSLAITDILLGLLVLPFSAIQ 76
QY 68 MGRRTSPAGACQVIGFLPTFLASNAALSAALSADQWLAVGFPRLRYAGRLPRYAGLL 127
Db 77 LSCKWSFGKVFNCIYITSLDVMCLTASILNLFMISLDRYCAVMDPLRYPLVTPARVAISL 136
QY 128 GCWAGSLAFSGAALGCSMLGYSS-----AFASCSRLRPPPEPRPFAAFTATLHAVGF 181
Db 137 VLIWVITSLFSLHGLWNSRNETSKGNHTTSKCNQVN-----EYGLVDGLVTF 188
QY 182 VLPFLAVLCLTSLQVHRVARRHCOQMDVTVMKALALADLHPSVORCLIQOQRHRATR 241
Db 189 YLPFLIMCITYIRFVARDQAKRIDHISSWKAATI-----REHRTV 231
QY 242 KIGIATATFLICFAPVYVMTRELAEVFPV-----TVNAQWGLSKCLTYSKAVADPFT 293
Db 232 TLAAVMGAFIICWFFY-----FTAFVYRGLRGDDAINEMLEAIVLWLGYSANLNPIL 284
QY 294 YSLLRPRFR---QVLAGMVHRLKRTPRPASTHDSLS-DVAGMVHQLLKRTPR 342
Db 285 YAALNRDFTGYQOL--FCRLANR-----NSHKTSLRNASQLSRTQSREPR 330
RESULT 4
US-09-473-634-13
; Sequence 13, Application US/09473634
; Patent No. 6440670
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; APPLICANT: Wright, Simon Ralph
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; TITLE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/09/473,634
; CURRENT FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 08/875,540
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: PCT/EP96/00397
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: GB9503866.7
; PRIOR FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-473-634-13
Query Match 12.7%; Score 236; DB 4; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;
QY 12 LVNVLAVALL----SNALVLLCCAYSABLRTRASGVLLVNLISGLHLLAALDMPFTLLGV 67
Db 18 ITVVLAVLITITVAGNVVCLAVGLNRRLR-NTNCFIVSLAITDILLGLLVLPFSAIQ 76
QY 68 MGRRTSPAGACQVIGFLPTFLASNAALSAALSADQWLAVGFPRLRYAGRLPRYAGLL 127
Db 77 LSCKWSFGKVFNCIYITSLDVMCLTASILNLFMISLDRYCAVMDPLRYPLVTPARVAISL 136
QY 128 GCWAGSLAFSGAALGCSMLGYSS-----AFASCSRLRPPPEPRPFAAFTATLHAVGF 181
Db 137 VLIWVITSLFSLHGLWNSRNETSKGNHTTSKCNQVN-----EYGLVDGLVTF 188
QY 182 VLPFLAVLCLTSLQVHRVARRHCOQMDVTVMKALALADLHPSVORCLIQOQRHRATR 241
Db 189 YLPFLIMCITYIRFVARDQAKRIDHISSWKAATI-----REHRTV 231

QY 242 KIGIATATFLICFAPVYVMTRELAEVFPV-----TVNAQWGLSKCLTYSKAVADPFT 293
Db 232 TLAAVMGAFIICWFFY-----FTAFVYRGLRGDDAINEMLEAIVLWLGYSANLNPIL 284
QY 294 YSLLRPRFR---QVLAGMVHRLKRTPRPASTHDSLS-DVAGMVHQLLKRTPR 342
Db 285 YAALNRDFTGYQOL--FCRLANR-----NSHKTSLRNASQLSRTQSREPR 330
RESULT 5
US-08-748-485-5
; Sequence 5, Application US/08748485
; Patent No. 5817480
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Goli, Surya K.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,485
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 791239
US-08-748-485-5
Query Match 12.5%; Score 232.5; DB 2; Length 359;
Best Local Similarity 22.0%; Pred. No. 2e-12;
Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;
QY 11 LVNVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISGLHLLAALDMPFTLLGVNRG 70
Db 24 ILIILITVTVAGNVVCLAVGLNRRLAS-LTNCFTIVSLAVTDLILLGLLVLPFSAIQ 82
QY 71 RTPAPGACQVIGFLPTFLASNAALSAALSADQWLAVGFPRLRYAGRLPRYAGLLGCA 130
Db 83 KWSFKVFCNIYITSLDVMCLTASILNLFMISLDRYCAVMDPLRYPLVTPARVAISL 142
QY 131 WGQSLAFSGAALGCSMLGY-----SSAFASCSRLRPPPEPRPFAAFTATLHAVGVLP 184

Db 143 WVISITSLFSLHGLWNSRNETSKDNTIVKCKQVNN-----EYGLVDGLVTYFLP 194
QY 185 LAVCLTSLQVHRVARHCQMDTV-TMKALALLADLHPSVRQCLIQCKRRHRATRKI 243
Db 195 LLIMCITYFRIFKIAREQARRINHGSKAATI-----REHKATVTL 236
QY 244 GIAIATFLICFAPYVMTLAEVLV-----TVNAQWGLSKCLTYSKAVADPTYS 295
Db 237 AAVMGAFICFPY-----FTVYVYGLKGDADVNEFEDVVLWGLYANSALNPLIYA 289
QY 296 LLRRFPQVLGAMVHRLKTRTPASTHSSSL 327
Db 290 ALNRDRTA---YHQLPCCRASHNSHETSLSL 317
RESULT 6
US-08-120-601B-8
; Sequence 8, Application US/08120601B
; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120.601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-120-601B-8
Query Match 12.5%; Score 232.5; DB 3; Length 391;
Best Local Similarity 24.5%; Pred. No. 2.3e-12;
Matches 78; Conservative 62; Mismatches 130; Indels 49; Gaps 11;
QY 2 GPGEALLAGLVVLA-VALLSNALVLLCCAYSALRTRASGVLLVNLGLHLLAALDM 60
Db 54 GQGSAILISFIVSVCLVGLGNSMVIYVILRYAKMT-ATNIVILNLAIADELL-MLSV 111
QY 61 PFTLLGVNRGTPSAPGACOVIGFLDTFLASNAALSVAALSADQWLVAGPLRYAGLRP 120
Db 112 PELVTSTLLRHWFFGALLCRLVSDVAYNMTSIVCLTVLSVDVRYAVVHPKAAVRRP 171
QY 121 RVAGLLLCGAWQS-----AFGGAALGCSWLGYSASFASCLRLPPPEPRPRAFT 173
Db 172 TVAKVNLGVWVLSLLVILPIVVFERTAN-----SDGTACNM-LMPEPAQRLWLVGFV 224
QY 174 ATLHAGVFLPLAVTCLTSLQVHRVARHCQMDTVTKALALLADLHPSVRQCLIQCK 233

Db 225 LVTFLMGFLFPVGAICL-----CYVLIATKQEWALKAGWQ-----QEK 263
QY 234 RRRHRATRKIGIAIATFLICFAPYVMTLAEVLV-----PFVTVNAQWGLSKCLTYSKAVAD 290
Db 264 RSRKITTLMVMVMVVFVVICWMPFVYVQVNVFAEQDDATVSQ-----LSVILGYANSCAN 319
QY 291 PFTYSLL-----RRPFRVL 305
Db 320 PLYGLFSLDNFRSPQRIL 338
RESULT 7
US-08-444-734A-6
; Sequence 6, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
; TITLE OF INVENTION: receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; TITLE OF INVENTION: cell lines
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92560
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FWI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-444-734A-6
Query Match 12.4%; Score 230.5; DB 1; Length 402;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEEALLAGLVVLAVALIS-----NALVLCCAYSALRTRASGVLLVNLGLHLLAAL 58
Db 34 PWEALLAGAL---LALAVLATVGGNLLVIAVAITPRLOT-MTNVFTVSLAADLVMGIL 89

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QY 59 DMPFTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRL 118
DB 90 VVPPAATLALTGHWPFGATGCELWTSVDVLCVTASITLCAVADRYLAVTNPLRYGALV 149
QY 119 RPYAGLLGCWAGQSLATSGAALGCSW--LGYSSAFASCSRLRPPPEPRFAAFTATL 176
DB 150 TKKARTAVLVVWVSAAVSFAPIMSQWVRVGDAAEQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVPLAVLCLTSLQVHRVARRHC-----QRMDTVTKKALA--- 215
DB 203 PYVLLSSVSFYLPLVWLFVYARFVVAQLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIQOKRRHRATKIGIAIATFLICFAPYVWTRL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRACTGLGIMGTFLCWLFFLANVLALGGPSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGMVHRLKRTPRP 319
DB 323 VGPAPFALN--W-----LGYNSAFNPLIYCRSPDPSAFRLLCRCGRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALFPFSGV 384

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RESULT 8

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US-08-087-772A-15
; Sequence 15, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Namias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Selzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-087-772A-15

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Query Match      12.4%; Score 230.5; DB 1; Length 402;
Best Local Similarity 24.9%; Pred. No. 3,5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

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QY 3 PGEALLAGLVMLAVALLS-----NALVLLCCAYSAELRTRASGVLLVNLGLHLLAAL 58
DB 34 PWEAALAGAL--LALAVLATVGNLLVIVAIATWPRLOQ--MTNVFVTSIAAADLVNGLL 89
QY 59 DMPFTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRL 118
DB 90 VVPPAATLALTGHWPFGATGCELWTSVDVLCVTASITLCAVADRYLAVTNPLRYGALV 149
QY 119 RPYAGLLGCWAGQSLATSGAALGCSW--LGYSSAFASCSRLRPPPEPRFAAFTATL 176
DB 150 TKKARTAVLVVWVSAAVSFAPIMSQWVRVGDAAEQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVPLAVLCLTSLQVHRVARRHC-----QRMDTVTKKALA--- 215
DB 203 PYVLLSSVSFYLPLVWLFVYARFVVAQLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIQOKRRHRATKIGIAIATFLICFAPYVWTRL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRACTGLGIMGTFLCWLFFLANVLALGGPSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGMVHRLKRTPRP 319
DB 323 VGPAPFALN--W-----LGYNSAFNPLIYCRSPDPSAFRLLCRCGRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALFPFSGV 384

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RESULT 9

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US-08-846-704-4
; Sequence 4, Application US/08846704
; Patent No. 6020157
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK J.
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-4

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Query Match 12.4%; Score 230.5; DB 3; Length 402;
Best Local Similarity 25.3%; Pred. No. 3.5e-12;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

QY 5 EALLAGLLVMVLAVALISNALAVLCCAYSAEIRTRASGVLLVNLISLGHLLAALDMPFTL 64
DB 46 EWVLIAYAVVFFVALVGVNTLVCLAVRNHHMRT-VTNYFVNLSDADVLTAVICLPASL 104
QY 65 LGVMRGRTSPAGCAQVIGFDLDTFLASNAALSVAALSADQWLAVGVFLRYAGRLPRYAG 124
DB 105 LVDITESWLFCHALKVIFLYQAVSVAVVLTLSFIALDRWYACHPELLFKSTAR-RARG 163
QY 125 LLIGCAWGQSALFSAALGCSWLGYSAFASCSRLPPEPERPFAA-----FTA 174
DB 164 SILG-INAVSLAI-----MVPQAAMVCSVLPPELANRTRLFVSDERWADDLYPK 213
QY 175 TLHVGFLVLP-LAVLCITSLQVHRVARRHCORMDVTVMKALA-----LLADL----- 220
DB 214 IYHSCFFITVTLAPLGLMAMAYFOIFKLGWQIQPGTTSALVRNWKPSQDGLDLEQGLS 273
QY 221 -HPSVRORCL---IQKRRHRATRKIGIAIATFLICFAP-----YVMTRLA--- 263
DB 274 GEPQPRARAFIAEVKQMRARAKTAKMLVMVLLVPALCYLPTSVLNLKRVFGMFQASDR 333
QY 264 ELVFPVTVNAQWGLSKCLTYSKAVADPFTYSLRRPRQVL-----AGVHRL 313
DB 334 BAVTACTTFSHW-----LVYANSAAPFIYNFLSGKFRQFQAAPSCCLPGLGPCGLK 387
QY 314 KRTPRPASTHDS 325
DB 388 APSPRESSASHKS 399

RESULT 10
US-07-916-901-2
; Sequence 2, Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
; APPLICANT: Granneman, James G.
; APPLICANT: Lahners, Kristine N.
; APPLICANT: Rao, Donald D.
; TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
; ADDRESSEE: MILTON
; STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,901
; FILING DATE: 19920720
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-324 (WSU)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-916-901-2
Query Match 12.4%; Score 230.5; DB 1; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

QY 3 PGEALLAGLLVMVLAVALIS-----NALVLLCCAYSAEIRTRASGVLLVNLISLGHLLAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAMTPRLQT-MTNVFTVTSAAADLWMLGL 89
QY 59 DMPEFTLLGVMRGRTSPAGCAQVIGFDLDTFLASNAALSVAALSADQWLAVGVFLRYAGRL 118
DB 90 VVPPAATLALGHWPGLGATGELTSDVLCTVASIETLCALAVDRLVAVTNPLEYCALV 149
QY 119 RPYRAGLLGCAWGQSALFSAALGCSW--LGYSAFASCSRLPPEPERPFAAFTATL 176
DB 150 TKRCARTAVLVVVVSAAVSFAPIMSQWRVGDAAEAORCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLPLAVLCITSLQVHRVARRHC-----QRMDVTVMKALA--- 215
DB 203 PTVLLSSVSFVLPPLVLMVLFYARVTVVATRLRLRGELGRFPPEPSPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIQKRRHRATRKIGIAIATFLICFAPYVMTRL-----AEL 265
DB 263 VGTCAPEGVPCAGRRPARLLPLREHRACTGLGLIMGTFTLCWLPFFLANVLRALGGPSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPFRQVLAGVHRLKTRPR 319
DB 323 VEGPAFLALN--W-----LGYSANFNLPLYCRSPDFRSLRLLCCGRRL---PPEP 371
QY 320 ASTHDSLSLDVAGM 332
DB 372 CAARPALFPSPGV 384

RESULT 11
US-08-450-962-2
; Sequence 2, Application US/08450962
; Patent No. 6274706
; GENERAL INFORMATION:
; APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
; APPLICANT: STROBERG, Donny
; TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KECK, MAHIN & CATE
; STREET: P.O. BOX 06110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606-0110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2" diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,962
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,829
; FILING DATE: 08-SEPT-1993
; APPLICATION NUMBER: 07/721,571
; FILING DATE: 25-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR89/00918
; FILING DATE: 25-JAN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleit, Martin; Gollin, Michael A.
; REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
US-08-450-962-2

Query Match 12.4%; Score 230.5; DB 3; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVMVLAVALLS-----NALVLLCCAYSAELRTRASGVLLVNLSLGHLILAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIATWTPRLQT-MTNVFTVSLAAADLVWGLL 89
QY 59 DMPFTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADOMLAVGFFLRYAGRL 118
DB 90 VVPPAATLALTGHWPGLGATGCELTSTVDVLCVTAETLCAVADRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAWGOSLAFSGAALGCSW--LGYSSAFASCSLRLPEPPEPRFAAFTATL 176
DB 150 TKRCARTAVLVVWVSAVSPFAPIMSQWVRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLPLAVCLTSLQVHRVARRHC-----QRMDTVTMKALA--- 215
DB 203 PYVLLSSVSFYLLVMLFVYARVFWATQRLRLRGELGRFPPEPSPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLTQKRRHRATKIGIAIATFLICFAPYVMTL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFLCWLPPFLANVLALGGPSL 322
QY 266 VP---FVTVAQWGLSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGWHRLKRTPRP 319
DB 323 VPGPAFLALN--W-----LGYANSAFNPLIYCSPDFRSFAFRLLRCGRRL---PPEP 371
QY 320 ASTHSSSLDVAGM 332
DB 372 CAARPALEPFGV 384

RESULT 12
US-08-450-962-5
Sequence 5, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
US-08-450-962-5
Query Match 12.4%; Score 230.5; DB 3; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVMVLAVALLS-----NALVLLCCAYSAELRTRASGVLLVNLSLGHLILAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIATWTPRLQT-MTNVFTVSLAAADLVWGLL 89
QY 59 DMPFTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADOMLAVGFFLRYAGRL 118
DB 90 VVPPAATLALTGHWPGLGATGCELTSTVDVLCVTAETLCAVADRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAWGOSLAFSGAALGCSW--LGYSSAFASCSLRLPEPPEPRFAAFTATL 176
DB 150 TKRCARTAVLVVWVSAVSPFAPIMSQWVRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLPLAVCLTSLQVHRVARRHC-----QRMDTVTMKALA--- 215
DB 203 PYVLLSSVSFYLLVMLFVYARVFWATQRLRLRGELGRFPPEPSPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLTQKRRHRATKIGIAIATFLICFAPYVMTL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFLCWLPPFLANVLALGGPSL 322
QY 266 VP---FVTVAQWGLSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGWHRLKRTPRP 319
DB 323 VPGPAFLALN--W-----LGYANSAFNPLIYCSPDFRSFAFRLLRCGRRL---PPEP 371
QY 320 ASTHSSSLDVAGM 332
DB 372 CAARPALEPFGV 384
RESULT 13
US-08-848-631-2
Sequence 2, Application US/08848631
Patent No. 6635442
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: MOUSE a3-ADRENERGIC RECEPTOR
GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.

US-09-479-128-2
; Sequence 2, Application US/09479128
; Patent No. 6319710
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-001
; CURRENT APPLICATION NUMBER: US/09/479,128
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 12.4%; Score 230.5; DB 4; Length 425;
Best Local Similarity 25.3%; Pred. No. 3.7e-12;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

QY	5	EALLAGLMMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPFTL	64
Db	46	EWLLIAAYVAVFVVALVGNLTLCIAWNNHMET-VTNYFVNLADVLVTAICLPASL	104
QY	65	LGVMEGRTPSAPGACQVIGFLDTFLASNAALSVAAALSADQMLAVGFFPLRYAGRPRVAG	124
Db	105	LVDITESMLFGHALCKVIPYLOAVSVAVLTLSFIALDRWYAIChPLLFKSTAR-RARG	163
QY	125	LLLCGANGCSLAFSGAALGCSWLGYSASFASCSLRLPPEPRPFAA-----PTA	174
Db	164	SLTG-IWAVSLAI-----WVQAAVMECSVLPELANRTRLFVCDERWADDLYPK	213
QY	175	TLHAVGVFLP-LAVLCTSLQVHRVARHCQMDTVMKALA-----LLADL-----	220
Db	214	IYHSCFFIVTYLAPLGLMAMAYFQIFRXLWGRIPIGTTLSALVRNWKRPDQGLDLEQGLS	273
QY	221	-HPSVRQRCLE---IQKRRHRHATRKIGIATATLICFAP-----YVMTFLA----	263
Db	274	GEFQPRARAFLEAVKQMRARRKAKMLMVLLLVFALCYLPISVLNVLKRVFGMFQASDR	333
QY	264	ELVPFVTVNAQWGLSKCLITYSKAVADPFTVSLRRPFRQVL-----AGMVHRL	313
Db	334	EAVYACFTFSHW-----LVYANSAANPIIYNFLSGKREQKAFSCCLPLGCPGCSLK	387
QY	314	KTPRPASTHDS	325
Db	388	APSPRSSASHKS	399

Search completed: May 18, 2004, 12:09:16
Job time : 24 secs